STIC-Biotech/ChemLib

67938

From: Sent: To: Subject:

Bunner, Bridget Tuesday, June 04, 2002 8:47 AM STIC-Biotech/ChemLib sequence search

Hi! I'd like the following sequence searched for case 09/655,272:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647 CM1-10D12 (703) 305-7148 mailroom 10C01

> Edward Hart Technica: Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher:
Phone:
Location:
Date Picked Up: 6/9/92
Date Completed: 6/4/60
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:/
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST(where applic.)
STN: ______
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16-OCT-2001
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 4 (TWIK related arachidonic acid-
          SEQUENCE FROM N.A.
                                                                         Homo sapiens (Human)
                                                                                         stimulated potassium channel protein) (TRAAK).
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PRINTS; PR01333; 2POREKCHANEL.
Ionic channel; Transmembrane; Ion transport; Potassium transport;
Glycoprotein; Alternative splicing.
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IPR000636; Cation_chan_non_lig.
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                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00520; ion_trans;
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InterPro; IPR002958; Occludin.
                                  1 MRSTTLLALLALVLLYLVSGALVFRALEOPHEOGAORELGEVREKFLRAHPCVSDQELGL 60
                                                1 MRSTTLLALLALVLLYLVSGALVFQALEOPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
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InterPro; IPR00636; Cation_chan_non_lig.
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EMBL; AF247042; AAF64062.1; ALT_INIT.
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FBBS Lett. 471:137-140(2000).
-IP FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTPORASSING CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
-IP SUBUNIT: HOMODIMER (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20499203; PubMed=11042359; Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M. Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S., "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore dommin potassium channel."; Brain Res. Mol. Brain Res. 82:74-83(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Assignment of KCNK4 encoding the human potassium channel TRAAK to chromosome 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Frontal cortex;
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                      PR01333;
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maingret F., Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                     Transmembrane; Ion transport; Potassium transport;
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                                                                                                         81.4%; Score 1692.5; DB 1; 82.4%; Pred. No. 1.9e-84;
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CYTOPLASMIC (POTENTIAL).
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p57789; 09H859;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ Channel subunit).
KUNKIO OR TREK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulations by polyunsaturated fatty acids, lysophospholipids and Gs, G1, and Gg protein-coupled receptors.";

J. Biol. Chem. 275:28398-28405(2000);

J. BIOLY CHANNEL PRODUCES RAPIDLY ACTIVATION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY ACTIVATION AND NON-INACTIVATION OUTWARD RECTIFIER K(+) CURRENTS. ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING UNSATURATED FREE FATTY ACIDS.

J. SUBCELLULAR LOCATION: Integral membrane protein (Potential).

J. SUBCELLULAR LOCATION: Integral membrane protein (Potential).

J. SUBCELLULAR LOCATION: INTEGRAL EXPRESSED IN PANCREAS AND KIDNEY AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE AND TO A LOWER LEVEL AN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lesage F., Terrenoire C., Romey G., Lazdunski M.; "Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                Pfam; PF00520; ion_trans; PRINTS; PR01333; 2POREKCH
                                                                                                                                                                                                                Interpro; IPR000636; Cation_chan_non_lig
Interpro; IPR001622; Channel_pore_K.
                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF279890; AAG15191.1;
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                                            Glycoprotein.
                                                                                                                                                                                                                                                                                                         InterPro; IPR003280;
                                                                                    Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIKEVADALGGGADPETNSTSNSSH-SAWDLGSAFFFSGTIITTIGYGNVALRTDAGRLF 119
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                                                                                                                                                                                                                                                                                                                                                 605873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                2POREKCHANEL.
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             71
                                                                                                                                                                                                                                                                                                         2poreK_channel
             CYTOPLASMIC (POTENTIAL).
                                                                                        Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND SMALL INTESTINE.
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Best Local
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DOMAIN
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
POCTassium channel subfamily K member 10 (Outward rectifying channel protein TREK-2) (TREK-2 K+ channel subunit).
KCNK10 OR TREK2.
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                                                                                                                                                                                                    Bang H., Kim Y., Kim D.; "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                               MEDLINE=20298807; PubMed=10747911;
                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                          family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 CIVEVTIPAVIEKYIEGWTALESIYEVVVTLTTVGEGDEVAGGNAGINYREWYKPLVWEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRSTTLLALLALVILLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                             UNSATURATED FREE FATTY ACIDS.
SUBCELLULAR LOCATION: Integral membrane
TISSUE SPECIFICITY: EXPRESSED MAINLY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELET 126
                                                                                                                                                               FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIQHALDADNAGVSP---IGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 183
                                                      CHANNELS
                                                                   AND TESTIS.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                  ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRIAGTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTA--RVTQR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPAYQPLVWFW 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CILYALFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAG
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154
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                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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51.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 790; DB 1;
Pred. No. 6.3e-36;
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PORE-FORMING 1 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LINKED (GLCNAC. . .) (POTENTIAL).
-LINKED (GLCNAC. . .) (POTENTIAL).
-LINKED (GLCNAC. . .) (POTENTIAL).
8EA615B08D147FBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (POTENTIAL)
                                                                                                  protein (Potential)
THE CEREBELLUM, SPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                          CURRENTS
                                                                                                                                                                                                                                                                                                                                                            potassium
                                                                                                    SPLEEN
                                                                                                                                                                      RAPIDLY
                                                                                                                                                                                                                                                                                             Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 152;
                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (Two-pore potassium channel TPKC1) (TREK-1 K-
         MEDLINE=97157476; PubMed=9003761;
                        TISSUE-Brain
                                SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                      Mus musculus (Mouse)
                                                                                                                                channel subunit).
                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                             CIW2_MOUSE
                                                                                                                       CNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01333; 2POREKCHANNEL. PRINTS; PR01499; TREKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF196965; AAF75132.1; -
                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                                                          121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 LIQHALDADNAGVSPV---GNSSNSSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [onic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 MKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHICVSPQELET 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                                                                                                                                                                                            CIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDEVAGGNAGINYREWYKPLVWFW
                                                                                                                                                                                                                                                                                                                                                                      CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGON-SPAYOPLVWFW
                                                                                                                                                                                                                                                                                                                                                                                                 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAG
                                                                                                                                                                                                                                                                                         ILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR 356
                                                                                                                                                                                                                                                                                                                 ILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTA--RVTQR 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00520; ion_trans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003976; Trek_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003280; 2poreK_channel.
IPR000636; Cation_chan_non_lig.
IPR001622; Channel_pore_K.
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72
154
182
203
234
263
299
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                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71
92
180
202
233
234
254
294
319
538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.9%;
51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 788; DB 1;
Pred. No. 8.1e-36;
                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PORE-FORMING 2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PORE-FORMING 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1FF33F0AA52B97E4 CRC64;
                                                                                                                                                                                                                           411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  243
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Qγ

Matches 142; Query Match

Conservative

56; Mismatches Score 770.5; DB 1; Pred. No. 5.4e-35;

84;

ω,.

Gaps

60

Length 411; Indels

Local Similarity

37.1%;

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CARBOHYD
SEQUENCE
                                CARBOHYD
                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The statement is no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                         DOMAIN
                                                                                                                                                                                                                                        PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01499; TREKCHANNEL.
                                                                                                                                                                                                                                                                                InterPro; IPR003280; 2poreK_channel.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001522; Channel_pore_K..
InterPro; IPR003976; Trek_channel.
                                                                                        DOMAIN
                                                                                                    FRANSMEM
                                                                                                                 NIAMOC
                                                                                                                                FRANSMEM
                                                                                                                                            NIAMOC
                                                                                                                                                         TRANSMEM
                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                Glycoprotein.
                                                                                                                                                                                                                                                                  Pfam; PF00520; ion_trans;
                                                                                                                                                                                                                                                                                                                                           MGD; MGI:109366;
                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: HOMODIMER (POTENTIAL).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED
                                                                                                                                                                                     PRANSMEM
                                                                                                                                                                                                                             Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99254548; PubMed=10321245; Patel A.J., Honore E., Lesage F., Fink M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                channels."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fink M., Duprat F., Lesage F., Reyes R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Neurosci. 2:422-426(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Inhalational anesthetics activate two-pore-domain background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lazdunski M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unconventional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, functional expression and brain localization of a novel unconventional outward rectifier K+ channel.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fink M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOFLURANE.
                                                                                                                                                                                                                                                                                                                                                     U73488; AAC53005.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15:6854-6862(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
                                                                                     1
47
129
157
178
208
238
273
294
           119
     A,
                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                         Kcnk2
                                                                                    46
67
155
177
207
228
228
268
293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
 45297 MW;
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
; 8F976DDD103EFA05 CRC64;
                                            REQUIRED
                                                        SENSITIVITY
                                                                  ESSENTIAL FOR CHLOROFORM AND HALOTHANE
                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                            POTENTIAL
                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                 POTENTIAL.
PORE-FORMING 1 (POTENTIAL).
                                                                                                 POTENTIAL
                                                                                                                                                         POTENTIAL
                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                             PORE-FORMING 2 (POTENTIAL)
                                                                                                                                                                                                                         Ion transport; Potassium transport;
                                      FOR BASAL CHANNEL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Romey G., Heurteaux C.
             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
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RESULT 6
CIW2_HUMAN
ID CIW2_HIMAN
ID CIW2_HIMAN
ID CIW2_HIMAN
ID CIW2_HIMAN
ID COMP
I6-OCT
DT 16-OCT
CHANNE
CO CHANNE
CO KAMMMAI
RT CHANNE
RT CHANNE
RT CHANNE
RT SEQUEN
RX MEDLIN
RA PAICE
RT CHANNE
RT SEQUEN
RC TISSUE
RA PRICE
RL Nat. N
RA PRICE
CC -!- FU
CC -!- FU
CC -!- SU

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIW2_HUMAN STANDARD; PRT; 426 AA.
095069; Q9UNE3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore potassium channel TPKC1).
KCNK2 OR TREK1 OR TREK.
                                Pfam; PF00520; ion_trans; 1. PRINTS; PR01333; 2POREKCHANEL. PRINTS; PR01499; TREKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databas -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99254548; PubMed=10321245;
Patel A.J., Honore E., Lesage F., Fink M.,
                                                                                                                                                                                                                                         MIM; 603219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              channels."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patel A.J., Honore E., Lesage F., F
"Inhalational anesthetics activate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                         InterPro;
                                                                                                                                                   InterPro;
                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN Buropean Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein (Potential).
MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH
CHLOROFORM, HALOTHANE AND ISOFLURANE.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMER (POTENTIAL).
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           channel;
                                                                                                                   IPR003280: 2poreK_channel.
IPR000636; Cation_chan_non_lig.
IPR001622; Channel_pore_K.
IPR003976; Trek_channel.
Transmembrane; Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Ve Catarrhini;
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Matches
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 5 (Acid-sensitive potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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DOMAIN
           "Cloning and expression of a novel pH-sensitive channel from human kidney.";
J. Biol. Chem. 273:30863-30869(1998).
                                                   Reyes R., Duprat F.,
Lazdunski M.;
                                                                                                                                                            channel protein TASK-2) (TWIK-related acid-sensitive KCNK5 OR TASK2.
                                                                                                                                                                                                                                       CIW5
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DOMAIN
                                                                         MEDLINE=99030343;
                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                     Homo sapiens (Human)
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                                                                                     TISSUE=Kidney
                                                                                              SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=9606;
                                                                                                                               Mammalia;
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mes 140; Conser
FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS
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                                                                                                                                                                                                                                       HUMAN
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                                                                                                                              Eutheria;
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                                                                                                                                        Chordata;
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49.1%;
                                                              Lesage F.,
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Pred. No. 2.2e-34;
Pred. No. 2.3e-34;
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S -> N (IN REF. 2).
A -> T (IN REF. 2).
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N-LINKED (GLCNAC. ..)
MISSING (IN REF. 2).
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                                                              Fink M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                      315 VVEPAGRPGSPAPAEKVETPSPPTASALDYPSENLAFIDESSDTQSERGCALPRAP
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                                                                                                                                                                                                                                                                                                                                           69 LGGGANPETSWTNSSNHSSAWNLGSAFFFSGTITTIGYGNIVLHTDAGRLFCIFYALVG
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                                                                                                                                                                                                                                                                                                                                                                                                      9 LLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIKLLVEA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K+ CONCENTRATIONS.
SUBGULT: HOMODIMER (POTENTIAL).
SUBCELLULLAR LOCATION: Integral membrane protein (Potential).
SUBCELLULLAR LOCATION: EXPRESSION IN KIDNEY, ALSO DETECTED TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
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                                                                                                                                                                                         VLVHLVIPPFVFMVTEGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELW
                                                                                                                                                                                                                      CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPA-YQPLVWFW
                                                                                                                                                                                                                                                  VPLCLTWISALGKFFGGRAKRLGQFLTKRGVSLRKA-----
                                                                                                                                                                                                                                                                                                                AGQG - - - - VAITGNQTFNN - WNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                  DVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGETGPGPGLGPQGGGLPALPPSL--VPL
                                                                                                                                                           ILFGLAYFASVLTTIGNWL-----RAVSRRTRA-----EMGGLTAQAASWTGTVTA-
                                                                                                                                                                                                                                                                                  IPL----FGMLLAGVGDRLGSSL-RRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG
                                                                                                                                                                                                                                                                                                                                                                        LTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDA
                                                                                                                             IYLGLAW----LSLFVNWKVSMFVEVHKAIKKRRRRKESFESSPHSRKALQVKGSTASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00520; ion_trans;
                                                                                                                                                                                                                                                                                                                                                                                                                                       115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000636; Cation_chan_non_lig
IPR001622; Channel_pore_K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
       -VPTLEEVSQTLRSKGHVSRSPDEE----AVARAP
                                                                                                                                                                                                                                                                                                                                                                                                                                      66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
; E871A7A4823DDA00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 6.7e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PORE-FORMING 1 (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
PORE-FORMING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
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                                                                                                                               286
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RESULT 8
CIW6_HUMAN
Q9Y257; Q9HB47;
16-OCT-2001 (Re
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
10-MAR-2002 (Rel. 41, Last annotation update)
Potassium channel subfamily K member 6 (Inward rectifying potachannel protein TWIK-2) (TWIK-originated similarity sequence).
KCNK6 OR TWIK2 OR TOSS.
                                                                                                      This SWISS-PROT entry is copyright. It is produced throu between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 275:28722-28730(2000).
-!- FUNCTION: Exhibits outward rectification in a physiological K(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mehta Y., Forsayeth J.R., Yost C.S.; J. Biol. Chem. 274:24440-24440(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J., Mehta Y., Forsayeth J.R., Yost C.S.; "TWIK-2, a new weak inward rectifying member of the tandem pore potassium channel family."; J. Biol. Chem. 274:7887-7892(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saganich M., Rudy B., Artman M., Coetzee W.A.; "Identification and cloning of TWIK-originated similarity (TOSS): a novel human 2-pore K+ channel principal subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Honore E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99175162; PubMed=10075682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 450:191-196(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20435832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF CYS-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pountney D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99285568; PubMed=10359073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "TWIK-2, an inactivating 2P domain K+ channel.";
                                                                                                                                                                                                                     LOWEST EXPRESSION DETECTED IN BRAIN.
MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND,
DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF PO
                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein (Potential).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (Shown here) and 2; are
produced by alternative splicing.
TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES
TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER (POTENTIAL)
                                                                                                                                                                                                      CHANNELS.
                                                                                                                                                                                                                                                                                           PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gradient and mild inward rectification in symmetrical K(+)
                 AF134149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       =20435832; PubMed=10887187;
.J., Maingret F., Magnone V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gulkarov I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
               AAD22980.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISOFORMS 1 AND 2), AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vega-Saenz de Miera E., Holmes
                                                                                                                                                               It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fosset M., Lazdunski M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Inward rectifying potassium
                                                                                                       There are no restrictions ong as its content is in
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                                                                                          Usage
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                                                                                            and
                                                                                                                                                                                                                       POTASSIUM
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                                                                                                                                                                                                                                         ND, TO A SMALL OR BARIUM.
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                                                                                            commercial
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AAD24000.1;

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RESULT 9
CIW1_HUMAN
ID CIW1_H
AC 000180
DT 16-OCT
DT 16-OCT
DT 16-CT
DT 6-CT
DT 16-CT
DT 16-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                        CIWI_HUMAN STANDARD; PRT; 336 AA.

000180; Q13307;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 1 (Inward rectifying potassium channel protein TWIK-1) (Potassium channel KCNO1).

KCNKI OR TWIKI OR HOHOI OR KCNO1.
                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                  Homo sapiens
     MEDLINE-96183184; PubMed-8605869
                              TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290
                                                  SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161
                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AFVERVLAAGRIGRVVLANASGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRSTTLLA-LLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFIKLLVEALGGGANPETSWTNSSNHSS-AWNLGSAFFFSGTIITTIGYGNIVLHTDAGR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRRGALLAGALAAYAAYLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPLVWFWILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLT---AQAASWTGTVTARVTQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALLGVVVTVCFLVPAVIFAHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLIGCLLFV--LTPTFVFSYM-ESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPA-Y 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVDILGPOPESHOOLSASS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTGPSAPPPEKEQPLLPSS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVLVTVYLFLGLVAMVLVLQTF - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR01096;
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ipR001622; Channel_pore_K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
313 AA;
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257
79
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                                                                                                                                                                                  (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ion_trans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWIK1CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33747 MW;
                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.6%; Score 386; DB 1; 34.8%; Pred. No. 1.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POT N-LINKED (GLCNAC. . .) (POT MISSING (IN ISOFORM 2). C->A: NO CHANNEL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PORE-FORMING 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PORE-FORMING 2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ion transport; Potassium transport;
                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1379382DFB0575DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RHVSDLHGLTELILLPPPCPASFNADEDD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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В

18 RSAWCFGFLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQ 77

RSTTLLALLAL-VLLYLVSGALVFQALEQPHEQOAQKKMDHGRDQFLRDHPCVSQKSLED

9

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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=98026667; PubMed=9362344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.; "Sequence and function of the two P domain potassium channels: implications of an emerging superfamily."; J. Mol. Med. 76:13-20(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND REVIEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 15:1004-1011(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barhanin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lesage F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98122696; PubMed=9462864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissuE=Brain;
                                                                                                                                                                                                                                                                                                                                                      EMBL; U33632; AAB01688.1; -. EMBL; U76996; AAB97878.1; -. EMBL; U90065; AAB51147.1; -. MIM; 601745; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                       Pfam; PF00520; ion_trans; 1.
PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                 InterPro; IPR003280; 2porel
InterPro; IPR000636; Cation
InterPro; IPR001622; Channe
InterPro; IPR001779; TWIK1
                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   Glycoprotein.
                                                                                                                                                                                                                                            Ionic channel; Transmembrane; Ion transport; Potassium transport;
                                                                                                                                                                                                                                                             PRINTS;
                                                                  SEQUENCE
                                                                                             CARBOHYD
                                                                                                          DOMAIN
                                                                                                                                    DOMAIN
                                                                                                                                                 TRANSMEM
                                                                                                                                                               DOMAIN
                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                      DOMAIN
                                                                                                                         TRANSMEM
            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND
BRAIN AND LOWER LEVELS IN PLACEBYTA, LUNG, LIVER AND KIDNEY.
BRAIN AND LOWER LEVELS IN PLACEBYTA, LUNG, LIVER AND KIDNEY.
MISCELLANEOUS: INHIBITED BY BARTUM, QUININE, QUINIDINE AND
INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHANNELS.
                                                                                                                                                                                                                                                             PR01096; TWIK1CHANNEL
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,
                                                                   336
  Conservative
                                                                   ΑA;
                                                                                  20
41
130
153
177
198
238
238
2367
336
                                                                     38143
               18.3%;
                                                                                                                                                                                                                                                                                                                     Channel
                                                                                                                                                                                                                                                                                                                                           2poreK_channel
                                                                                                                                                                                                                                                                                                                                 Cation_chan_non_lig
                                                                      ME.
    54;
                                                                                                                                                                                                                                                                                                       Channer.
                                                                                                                                                                                                                                                                                                                     _pore_K.
                 Score 379.5; DB Pred. No. 4.2e-14
                                                                     N-LINKED (GLCNAC. . .) (POT
T->A: NO EFFECT ON CHANNEL
; 2A41D9501323215D CRC64;
                                                                                                                                                    CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                            PORE-FORMING 1 (POTENTIAL).
                                                                                                                                        PORE-FORMING 2 (POTENTIAL)
                                                                                                                                                                               POTENTIAL
  Mismatches
                               DB 1;
                              Length 336;
                                                                                    (POTENTIAL).
        23;
        Gaps
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RESULT 10
CINI_MAC
ID CINI_MAC
O08581
DT 16-OCT
DT 16-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                          -!- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse twik K+ channel gene.", FEBS Lett. 425:310-316(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arrighi I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J., "Structure, chromosome localization, and tissue distribution o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/SVJ; TISSUE=Liver; MEDLINE=98218573; PubMed=9559671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 402:28-32(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lesage F., L
Lązdunski M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT 2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 1 (Inward rectifying potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The structure, function and distribution of the mouse TWIK-1 K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97165959; PubMed=9013852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           008581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIW1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 YKIGITCYLLLGLIAMLVVLET 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 YQPLVWFWILFGLAYFASVLTT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 LGFVTVSCFFFI--PAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNOKFREL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: WEAK INWARDLY, RECTIFYING POTASSIUM CHANNEL.
SUBUNIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: Integral membrane protein (Potential).

TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESION IN BRAIN,
KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
EPIDLDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE
EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HICHEST EXPRESSION IN
CERBBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
                                                                                                                                                                                                                                                                         ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C. SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                     CONCEPTION. EXPRESSION STABILIZES AFTER DAY 8.
                                                                                                                                                                                                                                                                  CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --FLLIGCLLFVLTPTFVFSYME-SWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFH---IRWGFSKQVVAIVHAVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRLFCIFYALVGIPLFGMLLAGVGDRLGSSL-RRGIGHIEAIFLKWHVPPGLVRSLSAVL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLGRVLEASNYGVSVLSNASGNWN------WDFTSALFFASTVLSTTGYGHTVPLSDG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIKLLVEALGGG----ANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lauritzen I., Duprat F., Reyes R., Fink M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                  There are no restrictions on ong as its content is in no
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ORK1_
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                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
MEDLINE-97075152; PubMed=8917578; Goldstein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H.; "ORKI, a potassium-selective leak channel with two pore domains cloned from Drosophila melanogaster by expression in Saccharomy
                                                           TISSUE-Larva
                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                               Drosophila melanogaster (Fruit fly).
                                                                                                                                                              ORK1 OR CG1615
                                                                                                                                                                                                  16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                            Q94526;
16-0CT-2001
                                                                                                                                                                                                                                                    ORK1_DROME
                                                                                                                                                                                                                                                                 DROME
                                                                     SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=7227;
                                                                                                               Ephydroidea;
                                                                                                                                                                                     Open rectifier potassium
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                                                                                                                                                                                                                                                                                                              245 YKIGITCYLLLGLITMLVVLET 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF033017; AAC16973.1; -. MGD; MGI:109322; Kcnk1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                  --FLLIGCLLFVLTPTFVFSYME-SWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPA 231
                                                                                                                                                                                                                                                                                                                                                                                                            GKAFCIIYSVIGIPFTLLFLTALVQRVTVHVTRRPVLYFH---IRWGFSKQVVAIVHAVL 186
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(Rel. 40, Last seq.
(Rel. 40, Last anno
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                                                                                                          Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Ion transport; Potassium transport;
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34.08;
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Last annotation updat
                                                                                                                                                                             channel protein 1 (Two pore domain potassium
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Pred. No. 1.4e-13;
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guban P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Karft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Parcleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Williams S.M., Woodage T., Worley K.C., Wang A.H., Wang X.,

RA Williams S.M., Woodage T., Worley K.C., Wan D., Yang S., Yao Q.A.,

RA Williams S.M., Woodage T., Worley K.C., Wa D., Yang S., Yao Q.A.,

RA Yeb R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Gibbs R.A., Myers B. W., Rubin G.M., Venter I.,

RA Gibbs R.A., Myers B. W., Rubin G.M., Venter J.C.,

RT The genome sequence of Drosophila melanogaster ";

CC ON EXTERNAL POTASSIUM CHANNEL RECTIFICATION IS DEPENDENT CC

CC ON EXTERNAL POTASSIUM CHANNEL RECTIFICATION IS DEPENDENT
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FlyBase; FBgn0017561; Ork1.
InterPro; IPR003280; 2poreK.channel.
InterPro; IPR001622; Channel.pore_K.
Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a cheween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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SIMILARITY: BEL
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BELONGS TO THE TWO PORE DOMAIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
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Glycoprotein

Ionic channel;

Transmembrane; Ion transport; Potassium transport;

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Best Local :
                                                                                                                                                                                         "TASK-3, a novel tandem pore domain acid-sensitive extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16650-16657(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9JL58;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequal 16-OCT-2001 (Rel. 40, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIW9
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK-3) (TWIK-related acid-sensitive K+ channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                Rajan S., Wischmeyer E., Liu
Karschin A., Derst C.;
                                                                                                                                                                                                                                                                                                                   MEDLINE=20287530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCNK9 OR TASK3.
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                                                                                                                                                                                                                                                                                                                                               CISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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                                                                                              SUBCELLULAR LOCATION: Integral STATITATION: RELONGS TO THE TWO
                                                                                                                                           CHANNEL PROTEIN
                                                                         CHANNELS
                                                                                                                                                                     FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILLLIFYISYLMFGAAIYYHIE-------HGEEKISRAEQRKAQIAINEY---LL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLSSNLKATQNRIWSG----VTKDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTTFAGRMIMIAYSVIGIPVNGILFAGLGEYFGRT----FEAIYRRYKKYKMSTDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLHTDAGRLFCIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTFGANQPKEFGGWFVVYQIFVIVWFIFSLGYLVMIMTFITRGLQS-----KKLAYLEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -HVPPGLVRSLSAVLFLLIGCLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EELGDKNTTTQDEILQRISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNI 111
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95; Conservative
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                                                                                                                                                                                                                                                                                                                   PubMed=10747866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WTGTVTARVTQRTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ANPETSWINSSNHSSAWNLGSAFFFSGTIITTIGYGNI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 353; DB 1; L; Pred. No. 3.1e-12; 54; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                          G.X., Preisig-Mueller R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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W; 09AE1A3669072E07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Hystricognathi; Caviic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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                                                                                              PORE DOMA
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                                                                                              rane protein (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Caviidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1001;
                                                                                                                                                                     BACKGROUND POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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                                                                                                   Q.
                                                                                                                                                                                                                                               channel.
                                                                                                                                                                                                                                                                                            Daut J.,
                                                                                                   POTASSIUM
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CIW3_MOUSE
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      SEE BE DI DI AC
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 104
KCNK3
       CIW3_MOUSE STANDARD; PRT; 409 AA.

035111; 035163;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 3 (Acid-sensitive potassin channel protein TASK) (TWIK-related acid-sensitive K+ channel)
(Cardiac two-pore background K+ channel) (CTBAK-1).

KCNK3 OR TASK OR CTBAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01333; 2POREKCHANEL. PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF212827; AAF63706.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                         SPISSVSP 347
                                                                                                                                                           APPAVVEP 318
                                                                                                                                                                             GEGGDI.Q-----
                                                                                                                                                                                                                                                                                                  MFYAVLGIPLTLVMFQSLGERMNTFVRYLLKRIKKCCGMRNTEVSMENMVTVGFFSCMGT
                                                                                                                                                                                                                                                                                                                                          LELVIL-
                                                                                                                                                                                                                                                                                                                                                                               LSLIACTFTYLLVGAAVFDALESDHEMREEEKL - - - KAEEIR - - - - IRGKYNISTEDYRQ
                                                                                                                                                                                                AEMGGLTAQAASWTGTVTARVTQRTGPS-----APPPE-----KEQPLLPSSL-----P
                                                                                                                                                                                                                                                           LCI---GAAAFSQCEEWSFFHAYYYCFITLTTIGFGDYVALQSKGALQRKPFYVAFSFMY
                                                                                                                                                                                                                                                                             LLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV--PGDGTGQNSPAYQPLVWFW
                                                                                                                                                                                                                                                                                                                     IFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGC
                                                                                                                                                                                                                                                                                                                                                           LLVEALGGGANPETSWINSSNHSSA--WNLGSAFFFSGIIITTIGYGNIVLHIDAGRLFC
                                                                                                                                                                                                                    ILVGLTVIGAFLNLVVLRFLTMNSDEERGEGEEGAALPGNPSSVVTHISEEARQVRQRYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00520;
                                                                                                                                                                                                                                                                                                                                                                                                                       104;
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003380; 2poreK_channel.
IPR000636; Cation_chan_non_lig.
IPR001622; Channel_pore_K.
IPR003092; TASK_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
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                                                                                                                                                                               SVCSCACYRSQPQNFGATLAPQPLHSISCRIEEISPSTLKNSLFP
                                                                                                                                                                                                                                                                                                                                                                                                                               16.0%;
28.3%;
                                                                                                                                                                                                                                                                                                                                         --QSEPHRAGVQWKFAGSFYFAITVITTIGYGHAAPGTDAGKAFC
                                                                                                                                                                                                                                        -----ASVLTTIGNWLRAVSRRTR
                                                                                                                                                                                                                                                                                                                                                                                                                       55;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 333.5; DB 1;
Pred. No. 1.3e-11;
5; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
PORE-FORMING 1 (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PORE-FORMING 2 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINKED (GLCNAC. . .) (P
261DC973FF53AF91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                310
                                                                                                                                                                                                                    287
                                                                                                                                                                                                                                                                              239
                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                      12;
         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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Kim D., Fujita A., Horio Y., Kurachi Y.;
"Cloning and functional expression of a novel cardiac two-pore
background K+ channel (cTBAK-1).";
Circ. Res. 82:513-518(1998).
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB013345; BAAZ8349
MGD; MGI:1100509; Kcnk3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., "TASK, a human background K+ channel to sense external near physiological pH.", EMBO J. 10:5464-5471(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S "Proton block and voltage gating are potassium-dependent in the cardiac leak channel Kcnk3.";
DOMAIN
                         TRANSMEM
                                                   DOMAIN
                                                                     TRANSMEM
                                                                                                  DOMAIN
                                                                                                                         TRANSMEM
                                                                                                                                                                          Glycoprotein.
                                                                                                                                                                                                                         PRINTS; PR01333; 2POREKCHANEI PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                                        Pfam; PF00520; ion_trans;
                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003280; 2poreK_channel.
InterPro; IPR000636; Cation_chan_non
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 4-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20287574; PubMed=10748056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                      DOMAIN
                                                                                                                                                                                                  Ionic channel;
                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97459932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODÍMER (POTENTIAL).

SUBCELLULAR LOCATION: Integral membrane protein (Potential).

TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DE
IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALI
INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLI
MISCELLANBOUS: INACTIVATED BY BARIUM.

SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O J. 16:5464-5471(1997).

FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.

WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                    ;; AB008537; BAA25436.1;
; AF241798; AAF81418.1;
; AF242508; AAF81418.1;
;; AF065162; AAG29339.1;
; AF006824; AAC53367.1;
;; AB013345; BAA28349.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
                                                                                                                                                                                                                                                                                               IPR003092;
                                                                                                                                                                                                                                                                                                                      IPR001622;
1
78
108
129
159
                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275:16969-16978(2000).
                                                                                                                                                                                                                                                   2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9312005;
29
101
128
128
158
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207
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Rodentia;
                                                                                                                                                                                                                                                                                                                      Cation_chan_non_lig.
Channel_pore_K.
                                                                                                                                                                                                                                                                                            TASK_channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED
                    CYTOPLASMIC (POTENTIAL)
POTENTIAL.
                                                                     PORE-FORMING POTENTIAL.
                                                                                                                         POTENTIAL
                                                                                                                                                 CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                               Ion transport; Potassium transport;
                                                                                                                                                 (POTENTIAL).
                                                                                               1 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pH variations
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RESULT
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               054912;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K+ channel).
                                                                                                                                                                                                                                                                 MEDLINE-98099797; PubMed-9437008; Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.; "An open rectifier potassium channel with two pore doma cloned from rat cerebellum."; J. Neurosci. 18:868-877(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIW3_RAT
                This
                                                                                                                                                                                                                                                                                                                                                              TISSUE-Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCNK3 OR TASK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE
EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AN
                                                                                                                                                                                                                    FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTAS CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
                                                            MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BUPIVACAINE AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A. SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                      OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT
                                              CHANNELS.
                                                                                                           SKELETAL MUSCLE.
                                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VAFSFVYILTGLTVIGAFLNLVVLR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWFWILFGLAYFASVLTTIGNWLRAVSRR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVSCISTLCIGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LALIVCTFTYLLVGAAVFDALESEPEMIERQRLEL-RQLELRARYNLSEGGYEELERVVL
SWISS-PROT entry is copyright.
een the Swiss Institute of Bio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            norvegicus (Rat).
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31.6%;
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

Q -> E (IN REF. 3).

V -> I (IN REF. 3).
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 Bioinformatics
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              It is produced through a collaboration
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                                                                                                                                                                                                                                      POTASSIUM
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EMBL outstation

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Best Local
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                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 9 (Acid-sensitive Potassium Potassium Channel :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF031384; AAC39952.1; ...
InterPro; IPR003280; 2poreK_channel.
InterPro; IPR003636; Cation_chan_non_lig.
InterPro; IPR001622; Channel_pore_K.
InterPro; IPR003092; TASK_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01333; 2POREKCHANEL. PRINTS; PR01095; TASKCHANNEL.
Rajan S., Wischmeyer E
Karschin A., Derst C.;
                        SEQUENCE FROM N.A. MEDLINE=20287530; PubMed=10747866;
                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                              Q9NPC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00520; ion_trans;
                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                        CIW9_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                          FVSCISTLCIGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQY---
                                                                                                                                                                                                                                                                         ----VAFSFVYILTGLTVIGAFLNLVVLR
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                                                                                                                                                                                                                                                                                                                                                                                                    VGIPLFGMLLAGVGDRLGSSLR------RGIG--HIEAIFLKWHVPPGLVRSLSAVLFL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTITTTIGYGNIVLHTDAGRLFCIFYAL 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      channel;
                                                                                                                  OR TASK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                          STANDARD;
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                                                                            Chordata;
Primates;
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31.6%;
             [X]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 332.5; DB 1;
Pred. No. 1.7e-11;
4; Mismatches 97;
              G.X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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PORE-FORMING 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PORE-FORMING 2 (POTENTIAL)
                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D2778016E09E2BF5 CRC64;
                                                                                                                                                                                                                                                                                                 264
              Preisig-Mueller R.,
                                                                                                                                                                                                          374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                              ----VSMANMVLIG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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Matches
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF212829; AAF63708.1;
EMBL; AF248241; AAG31730.1;
EMBL; AF279809; AAF85982.1;
EMBL; AF257080; AAG33126.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricted to the companion of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coetzee W., Rudy B.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Girard C., Lesage F., Tinel N., Lazdunski M.,
"Human Task-3, a novel 2P domain potassium ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M. Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.; "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel."; Brain Res. Mol. Brain Res. 82:74-83(2000).
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16650-16657(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ionic channel; Transmembrane; Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina M., Pountney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20499203; PubMed=11042359;
64 LLVEALGGGANPETSWTNSSNHSSA--WNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFC 121
                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHANNELS.
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                                                                                                                       LALLALVILYIVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQK----SLEDFIK 63
                                                                                                                                                                                                        107;
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                                                           LSLIVCTFTYLLVGAAVFDALESDHEMREEEKL---KAEEIR----IKGKYNISSEDYRQ 61
                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003380; 2poreK_channel.
IPR000636; Cation_chan_non_lig.
IPR001622; Channel_pore_K.
IPR003092; TASK_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   email to license@isb-sib.ch).
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42263 MW;
                                                                                                                                                                                                                      15.8%;
28.7%;
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                                                                                                                                                                                                 Score 327.5; I
Pred. No. 2.9e-
54; Mismatches
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8A19EAEE5A4D7F38 CRC64;
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POTENTIAL.
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ISPSTLKNSLFPS 349
                             PSPPTASALDYPS 346
                                                                                                                                                                                                                                                                                    IFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGC 181
                                                             EEPRPSRPRYKADVPDLQSVCSCTCYRSQDYGGRSVAPQNSFSAKLAPHYFHSISYKIEE 336
                                                                                             QRTGPSAPPPEKEQPLLPSSLPAP-PAVVEPAGRPGSP-----AP-----AEKVET
                                                                                                                         ILVG-----LTVIGAFLNLVVLRFLTMNSEDERRDAEERASLAGNRNS----MVIHIP
                                                                                                                                                         ILFGLAYFASVLTTIGNWLRAV------SRRTRAEMGGLTAQAASWTGTVTARVT
                                                                                                                                                                                        LCI----GAAAFSQCEEWSFFHAYYYCFITLTTIGFGDYVALQTKGALQKKPLYVAFSFMY
                                                                                                                                                                                                                      LLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV--PGDGTGQNSPAYQPLVWFW
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Search completed: June 4, 2002, 11:03:40 Job time: 204 sec

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OM protein - protein search, using sw model
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983_DAT:
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985_DAT:
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995_DAT:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 4 4 5 6 6 7 7 8 8 10	Result No.
2079 1692.5 1692.5 1692.5 1692.6 1688.5 1688.5 776.5 776.5 776.5	Score
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20 AAY3413 21 AAY94426 21 AAY94426 22 AAG67777 22 AAG67777 22 ABB12229 20 AAY34133 20 AAY34133 21 AAE10341 22 AAE10341 22 AAE10341	1
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ALIGNMENTS

RESULT

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AAY30647
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                                                                                                                                                                                                                                                    Mechanically sensitive potassium channel protein; TRAAK; mechanically sensitive potassium channel protein; TraAK; polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease; nervous system disease; epilepsy; cardiovascular disease, arrhythmia; nervous system disease; epilepsy; cardiovascular disease, arrhythmia; newrodegeneration; ischemia; anoxia; hormone secretion abnormality;
                                                                                                                                                                                                                                                                                                                    A mechanically sensitive potassium channel protein TRAAK.
                                                                                                                                                                                                                                                                                                                                               18-NOV-1999 (first entry)
                                                                                                                                                                                          WO9945108-A2.
                                                                                                                                                                                                                   Mus sp.
                                                                                                                                                                                                                                           muscular disease.
                                                                                                                                                                  10-SEP-1999.
                                                                                                                05-MAR-1998;
                                                              Honore E,
                                                                                      (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                           23-FEB-1999;
New mechanically sensitive potassium channel, used to screen for
                           N-PSDB; AAZ10606
                                        WPI; 1999-551038/46.
                                                              Fink M, Lazdunski M,
                                                                                                                    98FR-0002725.
                                                                                                                                             99WO-FR00404.
                                                                         Lesage F,
                                                                           Duprat
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Claim 2; Fig 1; 40pp; French.

specific modulators, potential therapeutic agents for heart and nervous

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                                                                                                                          Homo sapiens.
                                                                      WO200026253-A1
                                                                                                                                                psychiatric disorder; neurological disorder; Gene therapy.
                                                                                                                                                                                                                 Human; h-TRAAK; potassium channel polypeptide;
                                                                                                                                                                                                                                                                                    Human h-TRAAK polypeptide #1.
                                                                                                                                                                                                                                                                                                                                               04-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 LEGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTARVTQRTGPSAPPPEK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 CLLEVLTPTEVESYMESWSKLEAIYFVIVTLTTVGEGDYVPGDGTGQNSPAYQPLVWFWI 240
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                                                                                                                                                                            domain potassium channel; neurodegenerative disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 cllfvltptfvfsymeswsklealyfvivtlttvgfgdyvpgdgtgqnspayqplvwfwi 240
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100.0%; Pred. No. 4e-169;
tive 0; Mismatches 0
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AAY94426

AAY94426;

AAY94426 standard; Protein; 393 AA.

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                                          356 ergcplpraprgrrrpnpprkpvrprgpgrprdkgvpv 393
                                                                                                   361 ERGCALPRAPRGRRRPNPSKKPSRPRGPGRLRDKAVPV 398
                                                                                                                                           300 eqpl----1ppppcpaqplgrprspsppekaqppspptasaldypsenlafidessdtqs
                                                                                                                                                                                                                                                                         241 LEGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTARVTQRTGPSAPPPEK 300
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                                                                                                                                                                                                                                                                                                                                                   180 cilfvitptfvfcymedwskleaiyfvivtittvgfgdyvagadprqdspaygplvwfwi 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK polypucleotides from human tissue samples. h-TRAAK polypeptides have homology to the 2P domain potassium channel family of polypeptides. The h-TRAAK polypeptides and polypucleotides may be used in diagnostic assays for conditions related to h-TRAAK polypeptides and for identifying agonists and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and polynucleotides may also be useful for treatment and prevention (e.g. as vaccines) of certain diseases, such as pain, psychiatric disorders including depression and and head trauma and neurological disorders including Alzheimer's, stroke and head trauma and neurological disorders including migraine and antiponar who means the service of the service 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 21; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated h-TRAAK polypeptides belonging to the potassium channel family of polypeptides, useful for the diagnosis and treatment of h-TRAAK related disorders, e.g. depression and schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK polynucleotides from human tissue samples. h-TRAAK polypeptides have homology to the 2P domain potassium channel family of polypeptides. The h-TRAAK polypeptides and polynucleotides may be used in diagnostic assays for conditions related to h-TRAAK because the conditions related to h-TRAAK polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             schizophrenia, neurodegenerative disease including Alzheimer's, stroke and head trauma and neurological disorders including migraine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           imbalance and for identifying agonists and antagonists of h-TRAAK polypeptides and polynucleotides may also polypeptides. The h-TRAAK polypeptides and polynucleotides may also be useful for treatment and prevention (e.g. as vaccines) of certain diseases, such as pain, psychiatric disorders including depression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epilepsy. The present sequence is human h-TRAAK protein #2
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                                                                                                                                                                              121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180
                               181 CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI 240
301 EQPLLPSSLPAPPAVVEPAGRPGSPAPAEKVETPSPPTASALDYPSENLAFIDESSDTQS 360
                                                                                                                                                                                                                            61 likevadalgggadpetnstsnssh-sawdlgsafffsgtilttigygnvalrtdagrif 119
                                                                                                                                                                                                                                                               1
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                              1 mrsttliallalvilylvsgalvfraleqpheqqaqrelgevrekflrahpcvsdqelgl 60
                                                                                                                                                                                                                                                                                                                              1 MRSTTLLALLALVILYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-365583/31.
                                                                                                                                                                                                                                                               FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120
                                                                                                cifyalvgiplfgillagvgdrlgsslrhgighieaiflkwhvppelvrvlsamlfllig 179
                                                                                                                                                                                                                                                                                                                328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98GB-0024048.
99GB-0023668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-GB03634
                                                                                                                                                                                                                                                                                                                                                                                81.4%; Score 1692.5; DB 21; Length 393; 82.4%; Pred. No. 3.8e-136;
                                                                                                                                                                                                                                                                                                                                                                    24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
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Matches

Conservative

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AAG67777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG67777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG67777 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hormone secretion; cardiac disease; vascular disease; ischemia; nervous system disorder; endocrinal disease; muscle disease; retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; mechanically sensitive potassium channel; riluzole; TWICK,
                                                                                                                                     channel which is activated by polyunsaturated fatty acids (particularly channel which is activated by riluzole. The polypeptide is designated arachidonic acid (AA)) and by riluzole. The polypeptide is designated human TWICK-related AA-activated potassium channel (hTRAAK). The hTRAAK human TWICK-related on chromosome 11q13. HTRAAK is involved in regulation of neuronal and muscle excitation, cardiac rhythm and secretion of hormones. Cells that express hTRAAK, designated to screen for modulators hormones. Cells that express hTRAAK, designated to screen for modulators of hTRAAK activity. Such modulators are potentially useful for prevention of hTRAAK activity. Such modulators are potentially useful for prevention or treatment, in humans and animals, of: cardiac and/or vascular disease; or treatment, in humans and animals, of: cardiac and anoxia; endocrinal nervous system discorders associated with ischemia and anoxia; endocrinal diseases. Typical examples are epilepsy, cardiac arrhythmia and retinal diseases. Typical examples are epilepsy, cardiac arrhythmia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyunsaturated fatty acid; arachidonic acid; hTRAAK; chromosome 11q13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 ergcplpraprgrrrpnpprkpvrprgpgrprdkgvpv 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ERGCALPRAPRGRRRPNPSKKPSRPRGPGRLRDKAVPV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2000; 2000FR-0003264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuronal excitation; muscle excitation; cardiac rhythm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-2001; 2001WO-FR00758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200168670-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular diseases and in drug screening, is activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mechanically sensitive potassium channel, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAH78636, AAH78646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-590037/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a human mechanically sensitive potassium
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 34-35; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                          polyunsaturated fatty acids
                                                                                       Sequence
                                                                                                                            and neurodegeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lesage F, Maingret F;
              81.4%; Score 1692.5; DB 2
82.4%; Pred. No. 3.8e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 AA
24; Mismatches
                                         DB 22; Length 393;
      41;
        Indels
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                                                                                                                                                                       21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
20-JUN-2000; 2000US-0598042.
19-JUL-2000; 2000US-0520312.
31-AUG-2000; 2000US-0652450.
04-DEC-2000; 2000US-0729739.
 and diabetes -
           New G-protein-coupled receptor-like polypeptides and polynucleotides, useful for treating diseases of ophthalmic, neurological, immunologic
                                                                   N-PSDB;
                                                                                                                      Yamazaki V,
                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                human immunodeficiency virus; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; platelet disorder; thrombocytopaenia; aplastic anaemia; inflammatory disorder; septic shock; systemic inflammatory response yorder; septic shock; systemic inflammatory presponse syndrome; SIRS; hormonal dysfunction; cancer; atherosclerosis; wound; tissue regeneration; hamophilia; leukaemia; reperfusion injury;
                                                                                                                                                                                                                                                                   22-DEC-2000; 2000WO-US34983
                                                                                                                                                                                                                                                                                                     26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                           psoriasis; diabetes; h-TRAAK polypeptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkinson's disease; immunological disorder; HIV; candidiasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ophthalmic disease; neurological disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; G-protein coupled receptor like protein; GPCR; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human G-protein coupled receptor like protein, GPCR #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04571 standard; Protein; 1314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 ERGCALPRAPRGRRRPNPSKKPSRPRGPGRLRDKAVPV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 eqpl----1ppppcpaqplgrprspsppekaqppspptasaldypsenlafidessdtqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
       nephritic systems and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTARVTQRTGFSAPPPEK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 cifyalvgiplfgillagvgdrlgsslrhgighieaiflkwhvppelvrvlsamlfllig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                               2001-442255/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ergcplpraprgrrrpnpprkpvrprgpgrprdkgvpv 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQPLLPSSLPAPPAVVEPAGRPGSPAPAEKVETPSPPTASALDYPSENLAFIDESSDTQS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 g lay fas v lttignwlrvvsrrtraemggltaqaaswtgtvtarvtqragpaapppek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGONSPAYQPLVWFWI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG
                                                                    AAS08652
                                                                                                         Drmanac RT;
                                                                                                                        Tang YT
                                                                                                                     Liu
     hormonal dysfunction,
                                                                                                                   C,
                                                                                                               Zhou P, Wang
                                                                                                                Ď
cancer, atherosclerosis
                                                                                                             Zhang J,
                immunological
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ABB12229
                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a human G-protein coupled receptor (GPCR)-like CC protein, found to be homologous to human h-TRAAK polypeptide #1.

CC The GPCR-like polypeptides and polynucleotides are useful for the treatment of diseases of ophthalmic, neurological (e.g Alzheimer's CC disease and Parkinson's disease, immunological (e.g HIV infection and CC lupus erythematosus and rheumatoid arthritis), platelet disorders (e.g upus erythematosus and aplastic anaemia), inflammatory disorders (e.g cc septic shock and systemic inflammatory response syndrome, SIRS) and CC septic shock and systemic inflammatory response syndrome, SIRS) and CC cancer, atherosclerosis, wounds, tissue regeneration, haemophilia, CC cof each type of disorder are given in the specification. Anti-GPCR-like CC protein antibodies are useful for detecting or quantitating the CC polypeptide in tissue. The polypeptides can also be used as molecular weight markers and as a fond sunniament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                 haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                       Human K channel TRAAK homologue, SEQ ID NO:2599.
                                                                                                                                                                                                                         11-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                           ABB12229;
                                                                                                                                                                                                                                                                                                             ABB12229 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                         895 ergcplpraprgrrrpnpprkpvrprgpgrprdkgvp 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ERGCALPRAPRGRRRPNPSKKPSRPRGPGRLRDKAVP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     779 llglayfasvlttignwlrvvsrrtraemggltaqaaswtgtvtarvtqragpaapppek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 LFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTARVTQRTGPSAPPPEK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           659 cifyalvgiplfgillagvgdrlgsslrhgighieaiflkwhvppelvrvlsamlfllig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHYPPGLVRSLGAVLFLLIG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600 likevadalgggadpetnstsnssh-sawdlgsafffsgtiittigygnvalrtdagrlf 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 mrsttllallalvllylvsgalvfraleqpheqqaqrelgevrekflrahpcvsdqelgl 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         weight markers and as a food supplement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 203-208; 259pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGKLF 120
                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRSTTLLALLALVLLYLVSGALVFQALEOPHEQOAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eqpl----lppppcpaqplgrprspsppekaqppspptasaldypsenlafidessdtqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQPLLPSSLPAPPAVVEPAGRPGSPAPAEKVETPSPPTASALDYPSENLAFIDESSDTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cllfvltptfvfcymedwsklealyfvivtlttvgfgdyvagadprgdspayqplvwfwi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.2%;
82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1688.5; DB 2:
Pred. No. 3.7e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          838
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Best Local Similarity

70.3%; 18;

Pred. No. 4.5e-68; Mismatches

19;

Indels

40;

Gaps

182;

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cc giving an insight into their probable biological activities, and hence cg potential therapeutic applications. The polypeptides of the invention may continuous activities, including cytokine, cell proliferation or cell califerentiation activities; stem cell growth factor activity; confimunomodulatory activity; activity; tissue growth activity; chaematopolesis regulatory activity; tissue growth activity; chaematopolesis regulatory activity; tissue growth activity; chaematopolesis regulatory activity; tissue growth activity; chaematopolesis receptor or ligand activities; or may be conditions or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, carterial ischaemia, bone disorders (e.g., myeloid or lymphoid cell vascular growth. Polypeptides involved with tissue regeneration and creating (e.g., of burns, inclusions and ulcers), while those with a companial condition and conditions and ulcers), while those with conditions in addition to immune disorders. Comminuate stem cells in culture to give rise to neuroepithelial cells can be used to augment or replace cells damaged by illness, and nucleotides an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 318; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human proteins and DNA encoding sequences useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-2001; 2001WO-US03800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-457740/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA09473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer
                                                                                 The present sequence
                                                                                 represents a novel human
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RESULT
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AAY34133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY34133 standard; Protein; 411 AA.
                            This sequence represents the human K+Hnov59 potassium channel.

K+Hnov proteins have a high degree of homology to known potassium channels and may be alpha subunits, which form the functional channel, or accessory subunits that act to modulate the channel activity. K+Hnov59 is a 4 transmembrane domain, 2 pore domain potassium channel. The gene is located on chromosome 19, determined via PCR chromosomal localisation using primers AAZ11939 and AAZ11940. K+Hnov cDNAs were isolated by extension of expressed sequence tags (ESTs) which were related but not identical to known human potassium channels. Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome; cardiovascular disorder; CNS disorder; renal disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human potassium channel K+Hnov59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
                                                                                                                                                                                                  Claim 3; Page 104-105; 112pp; English.
                                                                                                                                                                                                                                  with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
                                                                                                                                                                                                                                                 New nucleic acids encoding mammalian K+Hnov potassium channel proteins, useful for the diagnosis and treatment of episodic
                                                                                                                                                                                                                                                                                                      WPI; 1999-527591/44.
N-PSDB; AAZ11915.
                                                                                                                                                                                                                                                                                                                                                                                       (AXYS-) AXYS
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25-FEB-1998;
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 polymorphisms detected as sequence variants between multiple independent clones. Potassium channels have critical roles i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 hggrcretegsqvaprlpasplcpgygnvalrtdagrifcifyalvgipifgillagvgd 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 EAIYFVIVTLTTVGFGDYV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 RLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGCLLFVLTPTFVFSYMESWSKL
independent clones. Potassium channels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTI------- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eaiyfvivtlttvgfgdyv
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                                                                                                                                                                                                                                                                                                                                                       Hu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0095836
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0116448
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                                                                                                                                                                                                                                                                                                                                                       Miller
                                                                                                                                                                                                                                                                                                                                                           ΑP,
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                                                                                                                                                                                                                                                                                                                                                         Rutter M,
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc cell types and biochemical pathways. Defective potassium channels are known to cause four human diseases: episodic ataxia with myokymia; cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome. CC cardiac arrhythmia (long QT syndrome); epilepsy; and sartter's syndrome. CC it is likely that abnormal potassium channels are also implicated in CC certain renal, cardiovascular and central nervous system (CNS) CC disorders. Nucleotides encoding K+Hnov proteins may be used for CC identifying homologous or related proteins and the DNA sequences encoding them. They may be used to produce compositions that modulate the CC expression and function of the K+Hnov protein and in studying the Diochemical pathways associated with it. They may also be used for the recombinant production of K+Hnov protein in fermentation cultures. CC Additionally, such nucleotides may be used in gene therapy protocols for the treatment of diseases associated with abnormal potassium channels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 142;
N-PSDB; AAZ00039
               WPI; 1999-469126/39
                                              Chapman CG, Meadows HJ;
                                                                                                                                                                                                                                                                                                               h-TREK1; two pore potassium channel; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                      h-TREK1 polypeptide
                                                                               (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                     27-JAN-1998;
                                                                                                                                   09-OCT-1998;
                                                                                                                                                                     02-DEC-1998;
                                                                                                                                                                                                        29-JUL-1999
                                                                                                                                                                                                                                     W09937762-A1
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                        chromosome 1q32
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAY28496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY28496 standard; Protein; 411 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lvglayfaavlsmigdwlrviskktkeevgefrahaaewtanvta 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 AA;
                                                                                                                   98EP-0300570.
                                                                                                                                   98GB-0022135
                                                                                                                                                                 98WO-EP07805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.3%; Score 776.5; DB 2
49.8%; Pred. No. 5.7e-58;
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             Lazdunski M,
                                         (CNRS ) CNRS CENT NAT RECH SCI.
                                                                         11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the h-TREKI polypeptide, encoded by the h-TREKI polypurcleotide AAX00039. h-TREKI is a two pore potassium channel, and the gene maps to human chromosome 1q32, between the markers D1S237 and WI5105. The polypurcleotide sequence of h-TREKI can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's, stroke, and head trauma and neurological disorders including migraine.
                                                                                          12-FEB-1999;
                                                                                                                    11-FEB-2000; 2000WO-IB00226
                                                                                                                                                       17-AUG-2000
                                                                                                                                                                                     WO200047738-A2
                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                             Human; potassium channel protein; TREK-1; anaesthetic; analgesia;
                                                                                                                                                                                                                                                                                             Human TREK-1 potassium channel protein.
                                                                                                                                                                                                                                                                                                                                 10-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                 AAE10341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 cvlfvalpaiifkhiegwsaldaiyfvvitlttigfgdyvaggsdieyldfykpvvwfwi 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New two pore potassium channel used for, e.g. treapulmonary, cardiovascular and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 ciiyallgiplfgfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRSTTLLALLALVILYIVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                         2000US-0503089
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                                                                                                                                                                                                                                                                                                                              (first entry)
          Honore E,
                                                                                          99US-0119727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.3%; Score 776.5; DB 2
49.8%; Pred. No. 5.7e-58;
          Lesage F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
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          Romey G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
          Patel AJ;
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RESULT 1
AAB50044
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XX AAB5
AC AAB8
XX AB9
DT 19->
XX Huma
XX Huma
KW Huma
KW neuu
KW neuu
KW atta
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XX OS Hom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analyesia in a mammal upon inhalation. The present sequence is human TREK-1
                                                                                                                          Homo
                                                                                                                                                                                        Human; TREK; 2P domain potassium channel; resting membrane potential; neuronal excitability; neurotransmitter release modulation; epilepsy; neurological disorder; sleep-related disorder; cognitive dysfunction;
              01-JUN-1999;
                                      01-JUN-2000;
                                                                     07-DEC-2000
                                                                                              WO200072863-A2
                                                                                                                                                    erectile dysfunction; alopecia
                                                                                                                                                                  Parkinson's chorea; Huntington's chorea;
                                                                                                                                                                               attention deficit disorder;
                                                                                                                                                                                                                                                   Human TREK
                                                                                                                                                                                                                                                                            19-MAR-2001
                                                                                                                                                                                                                                                                                                                                  AAB50044 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            219
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DB; AAD17496.
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                                                                                                                                                                                                                                                                                                                                  Protein;
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49.8%;
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                                                                                                                                                                              addiction; anxiety; phobia;
                                                                                                                                                                                                                                                                                                                                  411
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                                                                                                                                                                  cerebral
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                                                                                                                         Mechanically sensitive potassium channel protein; TREK-1; polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease; nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurological conditions such as epilepsy, sleep-related disorders, cognitive dysfunction, attention deficit disorder, addiction, anxiety/phobia, Parkinson's and Huntington's chorea, cerebral pals; incontinence, erectile dysfunction or alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of human TREK1 polypeptide, polynucleotides encoding them and modulators of h-TREK1 polypeptides for treating epilepsy, sleep-radisorders, addiction and dyskinesias including Parkinson's and
                                                                                                                                                                                               A mechanically sensitive potassium channel protein TREK-1
                                                      ds snw
                                                                                        neurodegeneration; ischemia;
muscular disease.
                                                                                                                                                                                                                                        18-NOV-1999
                                                                                                                                                                                                                                                                                                           AAY30648 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI 240
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                                                                                                                                                                                                                                                                                                           Protein;
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Pred. No. 5.7
                                                                                                          anoxia; hormone secretion abnormality;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mechanically sensitive potassium channel, used to screen for specific modulators, potential therapeutic agents for heart and nervous system disorders -
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ischemia or anoxia), abnormalities of hormone secretion and muscular disease. The protein itself may be used to treat these diseases. Antibodies specific for the protein are used to detect it in tissues also as therapeutic inhibitors or activators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a mechanically sensitive potassium channel protein designated TREK-1. The protein is activated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 23-25; 40pp; French
                      chromosome
                                 h-TREK1; two
                                                     Mouse h-TREK1 polypeptide.
                                                                             12-OCT-1999
                                                                                                                       AAY28497 standard; Protein; 411 AA.
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                              pore potassium
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                                                                                                                                                                                                                                                                                                                                                                                                            56; Mismatches
                                channel;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 770.5; DB 20; Pred. No. 1.6e-57;
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                             inflammatory disease;
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RESULT 13
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                                                 10-DEC-2001
                                                                                                AAE10342;
                                                                                                                                            AAE10342 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 26; 44pp; English.
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27-JAN-1998;
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Murine TREK-1 potassium channel protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
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98EP-0300570
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                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annel used for, e.g. trea
and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 770.5; DB:
Pred. No. 1.8e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 411;
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1:

amnesia

Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;

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RESULT 1
AAU07618
ID AAUC
XX
AC AAUC
XX
DT 21-N
XX
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DE Huma
XX
KW Tran
KW pest
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Best Local S
Matches 142
Transmembrane potassium ion channel protein; pest control; membrane potential; pesticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These can be induced in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analyesia in a mammal upon inhalation. The present sequence is murine TREK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
                                                                                                                                    AAU07618 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 32-33; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid encoding a TREK-1 potassium channel protein for
transfecting cells to be used to identify compounds with anesthetic
properties -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lazdunski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-1999;
11-FEB-2000;
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                                           Human potassium ion channel TPKC1 protein
                                                                            21-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                     61 FIKLLYEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                \verb|cliyallgiplfgfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfg|
                                                                                                                                                                                                                                                                                                                                                            CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG
                                                                                                                                                                                                                                                                     cvlfvalpavifkhiegwsaldaiyfvvitlttigfgdyvaggsdieyldfykpvvwfwi
                                                                                                                                                                                                             lvglayfaavlsmigdwlrviskktkeevgefrahaaewtanvta 323
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                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.1%; Score 770.5; DB 21; 49.8%; Pred. No. 1.8e-57; tive 56; Mismatches 84;
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inward potassium flux;
antihelminthic; nemato
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 nematode;
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AAU07622
ID AAU0
XX
AC AAU0
XX
DT 21-N
XX
DE Huma

21-NOV-2001

(first entry)

Human potassium ion channel TPKC1 mutant protein #1

RESULT

AAU07622 standard;

Protein;

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                                                                                                                                                                                                                                                                                                                                                                   Matches 140;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a mutant potassium ion channel protein, having four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-536570/59.
N-PSDB; AAS12169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a human transmembrane potassium ion channel protein, TPKC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 15; Page 45; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-2000; 2000US-0503849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BADI ) BASF CORP
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294 lvglayfaavlsmigrlvrviskktkeevgefrahaaewtanvta
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                                                                                                                                                                                                                                                                                                                             1 MRSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                                                                                    FIKLLVEALGGGANPETSWINSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120
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                                   LFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTA 285
                                                                      CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI
                                                                                                                                             ciiyallgiplfgfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfg
                                                                                                                                                                                 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180
                                                                                                                                                                                                                  liqqivaainagiip---lgntsnqishwdlgssfffagtvittigfgnisprteggkif
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                  36.5%; Score 759.5;
49.1%; Pred. No. 1.7
                                                                                                                                                                                                                                                                                                                                                                 57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  1.7e-56;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                               85;
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   338
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Query Match
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Matches 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-536570/59.
N-PSDB; AAS12181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents a human
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Local Similarity 48.8%;
hes 139; Conservative 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                    CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI 240
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                                                                                                         lvglayfaavlsmigrlvrviskktkeevgefrahaaewtanvta 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Ala replaced by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane potassium ion channel TPKC1 mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 755.5; DB 22; Length 426; Pred. No. 3.7e-56; 7; Mismatches 86; Indels 3;
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DЬ Qy

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Search completed: June 4, 2002, 11:00:13 Job time: 213 sec

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OM protein - protein search, using sw model
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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No.
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776.5
770.5
761.5
761.5
379.5
339.5
330.5
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2079
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Match Length DB
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Copyright (c) 1993 - 2000 Compugen Ltd
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d US-09-135-010A-116
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d US-09-135-011A-116
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Sequence 8, Appli
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Sequence 2, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
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                 Sequence 2, Appli
Sequence 114, App
Sequence 114, App
Sequence 80, Appl
Sequence 116, App
Sequence 2, Appli
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Query Best Match Qy Db Qy Db 1 Qy 1 Qy 1 Qy 1 Qy 1 Qy 1 Db 1	RESULT 1 US-09-236-C Sequence Patent N GENERAL APPLICAL APPLICAL APPLICAL TITLE OL TITLE OL FILE RET CURRENT CURRENT CURRENT NUMBER SEQ ID N ELENGTH TYPE: ORGANIL US-09-236-	28 32 32 32 33 33 33 33 34 44 44 44 54
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tch al Similarity 49.8%; Pred. No. 2.4e-57; al Similarity 49.8%; Pred. No. 2.4e-57; l142; Conservative 57; Mismatches 83; Indels 3; Gamestallallalvelyles 57; Mismatches 83; Indels 3; Gamestallallalvelyles 57; Mismatches 83; Indels 3; Gamestallallalvelyles 57; Mismatches 83; Indels 3; Gamestallallallallallallallallallallallallall	/09236080 ;242217el Compounds R: US/09/236,080 }-01-25 ndows Version 3.0	US-09-135-020-2 US-09-135-010A-2 US-09-634-920-2 US-08-194-338-5 US-08-26-138E-4 US-08-283-471A-28 US-09-283-471A-41 US-08-483-533-41 US-09-283-471A-41 US-09-283-471A-61 US-09-283-471A-61 US-09-283-471A-61 US-09-16-66 US-08-475-41A-66 US-08-475-41A-66 US-08-642-255-33 US-08-642-255-33 US-08-642-255-33 US-08-475-41A-66 US-08-642-255-33
Length 411; Indels 3; Gaps		Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli Sequence 28, Appli Sequence 41, Appli Sequence 41, Appli Sequence 61, Appli Sequence 66, Appli Sequence 160, Appli Sequence 66, Appli Sequence 66, Appli Sequence 66, Appli Sequence 66, Appli Sequence 66, Appli Sequence 66, Appli

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RESULT 2
US-09-36-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:

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APPLICANT: Duprat, Fabrice
APPLICANT: Luprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Lesage, Florian
APPLICANT: Lezdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989,6705C1P
CURRENT APPLICATION NUMBER: US/09/144,914
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1998-09-01
EARLIER FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: GR 96/01565
                                                                                                       US-09-144-914-8
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APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: G930031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 411
TYPE: DATE: DATE
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09144914 Patent No. 6309855
                                                                                                              FEATURE:
OTHER INFORMATION: TREK-1
                                                                                                                                                             ORGANISM: Murine
                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRSTTLLALLALVILYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
         36.68;
49.58;
Score 761.5; DB 4
Pred. No. 3.8e-56;
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                  DB 4;
              Length 370;
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; MOLECULE TYPE: US-08-749-816-2
Query Match
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                                                                                                       TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acid
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                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 98: TELECOMMUNICATION INFORMATION: TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                      FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY FACENT INFORMATION:
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
NIMBER OF CONTENTS. OF DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                               TOPOLOGY:
                                                                                                                                       TELEPHONE: 215-0, TELEPHONE: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                        NAME: Weiser, Gerard J
REGISTRATION NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTY: Philadelphia
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                                                                                           amino acids
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Guillemare, Eri
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                                                                                                                                                                                                                                                                                                     US/08/749,816
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Best Local Similarity

18.3%;

Score 379.5; DB 3; Pred. No. 3.4e-24;

Length 336;

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                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS FILE REFERENCE: 989.6705CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
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EARLIER APPLICATION NUMBER: FR 96/01565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 LGFVTVSCFFFI--PAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFREL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 --FLLIGCLLFVLTPTFVFSYME-SWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 YQPLVWFWILFGLAYFASVLTT 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 RSAWCFGFLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQ 77
176 --FLLIGCLLFVLTPTFVFSYME-SWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPA 231
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                                                                                          GKAFCIIYSVIGIPETLLELTAVVQRITVHVTRRPVLYFH---IRWGFSKQVVAIVHAVL 186
                                                                                                                                                                                                                                                                                RSAWCFGFLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQ 77
                                                                                                                                         GRLFCIFYALVGIPLFGMLLAGVGDRLGSSL-RRGIGHIEAIFLKWHVPPGLVRSLSAVL 175
                                                                                                                                                                                     FLGRVLEASNYGVSVLSNASGNWN-------WDFTSALFFASTVLSTTGYGHTVPLSDG 129
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                                                                                                                                                                                                                                                                                                                                                                          18.3%; Score 379.5; DB 4; Length 336; 34.4%; Pred. No. 3.4e-24; ative 54; Mismatches 95; Indels 23
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US-09-236-080-4
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                                                                                                                        ; OTHER INFORMATION: TASK US-09-144-914-5
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APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
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Best Local :
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APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
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                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS TITLE REPERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234
EARLIER APPLICATION NUMBER: 60/095,234
EARLIER FILING DATE: 1996-02-08
NUMBER: 0F SED ID NOS: 24
CORTMANDER: DETACHTO NUMBER: 67-02-08
NUMBER: OF SED ID NOS: 24
CORTMANDER: DETACHTO NUMBER: 67-02-08
Query Match 16.0%; Score 332.5; DB 4; Best Local Similarity 31.6%; Pred. No. 3.8e-20; Matches 85; Conservative 44; Mismatches 97;
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                                                                                                                                                                                             ORGANISM: Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFV 105
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                                                          DB 4; Length 405;
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; OTHER INFORMATION: TASK
US-09-144-914-4
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CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
FEARLIER FILING DATE: 1996-11-15
FEARLIER FILING DATE: 1996-02-08
FEARLIER APPLICATION NUMBER: FR 96/01565
FEARLIER FILING DATE: 1996-02-08
NUMBER: OF SEQ ID NOS: 24
SOFTWARE: PACENTIN VET. 2.0
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APPLICANT: LAZdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989.6705CIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
163 GFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQY-- 220
                                           180 G---CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV--PGDGTGQNSPAYQP 234
                                                                                      116 LGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRA------DVSMANMVLI 162
                                                                                                                             127 VGIPLFGMLLAGVGDRLGSSLR------RGIGHIEAIFLKWHVPPGLVRSLSAVLFLLI 179
                                                                                                                                                                           68 RLKPHKAGVQ------WRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYAL 115
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                         7 LALLALVILYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIKLLV 66
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                                                                                                                                                                                                                  EALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFYAL 126
                                                                                                                                                                                                                                                             LALIVCTFTYLLVGAAVFDALESEPELIERQRLEL-RQQELRARYNLSQGGYEELERVVL 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EALGGGANDETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFYAL 126
                                                                                                                                                                                                                                                                                                                                                                85; Conservative
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                                                                                                                                                                                                                                                                                                                                           15.7%; Score 326.5; DB 4; Leny...
31.5%; Pred. No. 1.2e-19;
45: Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 394;
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US-08-332-312-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08332312 Patent No. 5559026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Function
TITLE OF INVENTION: Melana
274 AQAAS-------WTGTVTARVTQRTG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                225 VPTFGANQPKEFGGWFVVYQIFVIVWFIFSLGYLVMIMTFITRGLQS------KKLAYLE 278
                                                                                        220 VPGDGTGQNSP-----AYQPLVWFWILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLT 273
                                                                                                                                165 HYVPPQLGLITTVVIALIPGIALFLVLPCVGVHLLRELGLSSISLYYSYVTTTTIGFGDY 224
                                                                                                                                                                                                            112 SPTTFAGRMIMIAYSVIGIPVNGILFAGLGEYFGRT-----FEAIYRRYKKYKMSTDM 164
                                                                                                                                                                      162 -HVPPGLVRSLSAVLFLLIGCLLFVLTPTF-VFSYMESWSKLEAIYFVIVTLTTVGFGDY 219
                                                                                                                                                                                                                                                      111 VLHTDAGRLFCIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKW------ 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                 67 EALGGG------ANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 LVWFWILFGLAYFASVLTTIGNWLRAVSRR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Harrington, James J
REGISTRATION NUMBER: P-38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                             7 LALLALVILYIVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIKILV 66
                                                                                                                                                                                                                                                                                                                                                                         7 ILLLIFYISYLMFGAAIYYHIE------HGEEKISRAEQRKAQIAINEY---LL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07470-8426
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                                                                                                                                                                                                                                                                                            EELGDKNTTTQDEILQRISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%; Score 301.5; DB 1; Length 618; 27.7%; Pred. No. 2.6e-17; tive 51; Mismatches 111; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Functional Expression of a Drosphila
Melanagaster Putative Potassium Channel in Yeast
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US-08-332-312-4
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                                                                                                   RESULT 11
US-08-749-816-4
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                                    Sequence 4, Application US/08749816 Patent No. 6013470 GENERAL INFORMATION:
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Best Local :
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
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APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Functional Expression of a Drosphila
TITLE OF INVENTION: Melanagaster Putative Potassium Channel in Yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
APPLICANT: Lesage, Florian APPLICANT: Guillemare, Eric
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                     188 MYIILLYIILG 198
                                                                                                                                                                                                                         233 QPLVWFWILFG 243
                                                                                                                                                                                                                                                                     144 VYTAFGGVLM-----
                                                                                                                                                                                                                                                                                                           174 VLFLLIGCLLFYLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVP-GDGTGQNSPAY 232
                                                                                                                                                                                                                                                                                                                                                                                             144 -----GSSLR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 SSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFYALVGIPLFGMLLAGVGDRL-- 143 ; | |: ||: ||: || || ; || : : | : :
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                                                                                                                                                                                                                                                                                                                                                                                                                                  25 TETWTFSSSIFFAVTVVTTIGYGNPVPVTNIGRIWCILFSLLGIPLTLVTIADLAGKFLS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
56; Conserv
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)GY: linear
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                                                                                                                                                                                                                                                                       -SKLEPWSEFTSFYWSFITMTTVGFGDLMPRRDG-----Y 187
                                                                                                                                                                                                                                                                                                                                                                                             -----RGIGHIEAIFLKWHVPPGLVRSLSA 173
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                                                                                                                                                                                                  RESULT
                  GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                Sequence 7, Application US/09144914 Patent No. 6309855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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APPLICANT: BATHANIN, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
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NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,
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LENGTH: 383 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              104 TKKLILMLEDAHNAHAFEYFFLNHEIPKDMWTFSSALVFTTTTVIPVGYGYIFPVSAYGR 163
                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                                                                                             179 IGCLLEV--LTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVP 221
                                                                                                                                                                                                                                                                                                                                                         164 MCLIAYALLGIPLTLVTMADTGKFAAQLVTRWFGDNN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: WEISER & ASSOCIATES STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 IKLLVEALGGGANP---ETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 LVLSCVTYALGGAYLFLSIEHPEELKRREKAIREFQDLKQQFMGNITSGIENSEQSIEIY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                   --CLLFAYPLVVGFILCSTSNITYLDSVYFSLTSIFTIGFGDLTP 252
                                                                                                                                                                                                                                                                                                                                                                                                    LFCIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%; Score 198; DB 3; Length 383; 26.7%; Pred. No. 6.5e-09; ative 42; Mismatches 95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234
EARLIER FILING DATE: 1998-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS FILE REFERENCE: 989.6705CIP
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/749,816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Unknown FEATURE:
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                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Romey, Georges
APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 --CLLFAYPLVVGFILCSTSNITYLDSVYFSLTSIFTIGFGDLTP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 IGCLLFV--LTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 MCLIAYALLGIPLTLVTMADTGKFAAQLVTRWFGDNN--------MAIPAAIFV- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 LFCIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLL 178
FILING DATE:
                                                                                                                                                                                                                                       CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 TKKLILMLEDAHNAHAFEYFFLNHEIPKDMWTFSSALVFTTTTVIPVGYGYIFPVSAYGR 163
                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 IKLLVEALGGGANP---ETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 LVLSCVTYALGGAYLFLSIEHPEELKRREKAIREFQDLKQQFMGNITSGIENSEQSIEIY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                             19102
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                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fink, Michel
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15-NOV-1996
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; OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog US-09-144-914-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ_ID_NO_6_.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09144914 Patent No. 6309855
                                                                                                                                                                                                                                       TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS FILE REFERENCE: 989.6705CIP CURRENT APPLICATION NUMBER: US/09/144,914 CURRENT FILING DATE: 1998-09-01 EARLIER FILING DATE: 1998-09-01 EARLIER APPLICATION NUMBER: 08/749,816 EARLIER FILING DATE: 1996-11-15 EARLIER APPLICATION NUMBER: 60/095,234 EARLIER FILING DATE: 1998-08-04
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                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: FR 96/01565 EARLIER FILING DATE: 1996-02-08
                                           ORGANISM: Unknown FEATURE:
                                                                                      TYPE: PRT
                                                                                                                 LENGTH: 347
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MOLECULE TYPE:
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TELEFAX: 215-875-8394
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NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 FLIGIGDIVPTN------LVWF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 QHDYLIFLS------SLLLCSISLLSSSALFSSIENISYLSSVYFGIITM 241
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RESULT 15
US-08-906-865-4
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US-08-906-865-4
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08906865
                                                                                                                                                                                                          TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
                                MOLECULE TYPE: pro
DESCRIPTION: /de
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
TYPE: amino acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,865
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 TTVGFGDYVPGDGTGQNSPAYQPLVWF 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 LTIFYSLLMIPVFIAFKFEFGTFLAHFLVVVSNRTRLAVKKAYYKLSONPENAETPSNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 FLIGIGDIVPTN-----LVWF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 --PIGGKITAEMKSKLGKCLTKSSRID---GFGKAIFFSWTLYSTVGYGSLYPHSTLGRY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 VEALGGGANPETS-----WTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 LSAAITLLVFNLI-GAGIFYLAETQNSSES------LNENSEVS-KCLHNL----
                ORGANISM:
                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LLALLALVILIYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIKLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 Hackensack Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                Homo sapiens
                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 David A. Jackson,
                                                                                          protein
                                                                       /desc = "Synapsin Ia"
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Continental Plaza,
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Best Local Similarity
585 QQRQGPPQKPPGPAGPTRQASQAGPV 610
                                    373 RRRPNPSKKPSRPRGPGRLRDKAVPV 398
                                                                              535 PVAGGPGAPPAARPPASPSP-----QRQAGPPQATRQTSVSGPAPPKASGAPPGG 584
                                                                                                                    319 -- AGRPGSPAPAEKVETPSPPTASALDYPSENLAFIDESSDTQSERGCALPRA----PRG 372
                                                                                                                                                            475 QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPQRLPSPTSAPQQPASQAAPPTQGQGRQSR 534
                                                                                                                                                                                                289 QRTGP---SAPPPEKEQPL-------LPSSLPAPPAVVEP----------- 318
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                              6.3%; Score 132; DB 3; Length 696; 28.8%; Pred. No. 0.0048;
                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                           Gaps
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Search completed: June 4, 2002, 11:00:34 Job time: 124 sec

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Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                         Database :
                                                                                                                               Post-processing: Minimum Match 0% Maximum Match 10
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein -
                                                                                                                                                                                   seq length: 0
seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   June 4, 2002, 10:58:45; Search time 20.89 Seconds (without alignments)
1830.711 Million cell updates/sec
                                                                                                           Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                         1 MRSTTLLALLALVLLYLVSG.....SKKPSRPRGPGRLRDKAVPV 398
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2079
                                                                            PIR_71:*
                                                                                                                                                                                                                                                                             283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
pir1:*
pir2:*
pir3:*
pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 4 4 5 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	2	Result No.
323.5 314.5 298.5 291.5 291.5 269.5 269.5 269.5 269.5 240.5 240.5 240.5 240.5 240.5 240.5 240.5 231.5 231.5 231.5 231.5 231.5 231.5 231.5	379.5	Score
15.6 15.1 14.4 14.4 13.0 13.0 12.9 12.7 12.6 11.6 11.7 11.5 11.5 11.5 11.5 11.6 11.6 11.7 11.7 11.7 11.7 11.7 11.7	18.3 17.0	Query Match L
330 329 336 336 336 528 392 523 523 523 513 513 1910 643 325 445 452 452 452 453 453 461 461 461 461 461 461 461 461 461 461	336	Length D
	22	B
TYC7703 TYC7703 TYC43361 TYC43361 TYC43361 TYC45032 TYC5392 TYC5392 TYC5392 TYC5392 TYC5392 TYC5392 TYC5392 TYC5392 TYC5616 TY	\$65566 T13807	Ĭ
TASK-5 protein probable potas; outward rectif. outward rectif. probable potas; hypothetical proportion proportion proportion proportion proportion proportion proportion protein T12C9. hypothetical proportion protein T12C9. hypothetical proportion protein protein protein protein protein protein protein twk-24 hypothetical proportion protein twk-24 hypothetical proportion protein p	inward r potassiu	Description
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	
192	193.5	194	197.5	198	199	201	202.5	204	205	205	210	211	213	216.5	218.5	
9.2	9.3	9.3	9.5	9.5	9.6	9.7	9.7	9.8	9.9	9.9	10.1	10.1	10.2	10.4	10.5	
405	757	586	569	383	681	381	1136	550	576	544	631	769	475	335	519	
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21188	T24266	21683	43531	T23746	19429	43393	26953	22557	43363	T43364	T26232	T27550	27725	S44635	T16629	
nypothetical proce			probable potassium	hypothetical proce	nypothetical proce	potassium channei	nypothetical proce	nypothetical proce	potassium channel	potassium channer	nypotherical proce	nypothetical proce		122D/./ protein -	hypothetical prote	

ALIGNMENTS

RESULT S65566

inward rectifier potassium channel TWIK-1 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S65566
R;Lesage, F; Guillemare, E; Fink, M.; Duprat, F; Lazdunski, M.; Romey, G.; Barhani
EMBO J. 15, 1004-1011, 1996

A;Title: TWTK-1, a ubiquitous human weakly inward rectifying K(+) channel with a nove A;Reference number: S65566; MUID:96183184
A;Accession: S65566

A;Cross-references: EMBL:U33632; NID:g1086490; PIDN:AAB01688.1; PID:g1086491

A; Molecule type: mRNA A; Residues: 1-336 <LES>

A; Status: preliminary

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Best Local Similarity 34.4%; Pred. No. 2.2e-17;
Matches 90; Conservative 54; Mismatches 95
                                                                              187 LGFVTVSCFFFI--PAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFREL 244
                                                                                                                                                                 130
                                                                                                                                                                                                          117
245
                                       232 YQPLVWFWILFGLAYFASVLTT 253
                                                                                                                                                                                                                                               78 FLGRVLEASNYGVSVLSNASGNWN------WDFTSALFFASTVLSTTGYGHTVPLSDG 129
                                                                                                                                                                                                                                                                                      61 FIKLLVEALGGG----ANPETSWINSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDA 116
                                                                                                                                                                                                                                                                                                                                18 RSAWCFGFLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQ 77
                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                     --FLLIGCLLFVLTPTFVFSYME-SWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPA 231
                                                                                                                                                              GKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFH----IRWGFSKQVVAIVHAVL 186
                                                                                                                                                                                                      GRLFCIFYALVGIPLFGMLLAGVGDRLGSSL-RRGIGHIEAIFLKWHVPPGLVRSLSAVL 175
                                                                                                                                                                                                                                                                                                                                                                       RSTTLLALLAL-VLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
YKIGITCYLLLGLIAMLVVLET 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                         95;
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potassium channel protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13807

RESULT T13807

R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H. Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A;Title: ORK1, a potassium-selective leak channel with two pore domains cloned from D.A;Reference number: Z17770; MUID:97075152

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Ωy
                                                                                                                                                                                        F;107-128/Nomain: transmembrane segment #status predicted <TMS2>
F;129-155/Region: hydrophobic cytoplasmic linker #status predicted
F;156-180/Domain: transmembrane segment #status predicted <TMS3>
F;220-240/Domain: transmembrane segment #status predicted <TMS4>
                                                                                                                                                                                                                                                                                        F;7-30/Domain: transmembrane segment #status predicted <TMS1>
                                                                                                                                                                                                                                                                                                                      A; Map position: 20q12
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: JC7703

R;Kim, D.; Gnatenco, C.

Biochem. Blophys. Res. Commun. 284, 923-930, 2001

A;Title: TASK-5, a new member of the tandem-pore K+ channel family.

A;Reference number: JC7703; MUID:21303050; PMID:11409881
                                                                                                                                                                                                                                                                                                                                                                              A; Gene: task-5
                                                                                                                                                                                                                                                                                                                                                                                                       C:Comment: This protein, a new member of the tandem-pore K+ channel family with four tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-330 < KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:AL118522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
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A;Cross-references: FlyBase:FBgn0017561
A;Map position: 1
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1001 <GOL>
                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Genetics
                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 PTFGANQPKEFGGWFVVYQIFVIVWFIFSLGYLVMIMTFITRGLQS-----KKLAYLEQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 HYVPPQLGLITTVVIALIPGIALFLLLPSWVFTYFENWPYSISLYYSYVTTTTIGFGDYV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 -HVPPGLVRSLSAVLFILLIGCLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 SPTTFAGRMIMIAYSVIGIPVNGILFAGLGEYFGRT-----FEAIYRRYKKYKMSTDM 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 VLHTDAGRLFCIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein - human
3 STTLLALLALVILVIVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 EALGCG------ANPETSWTNSSNHSSAWNLGSAFFFSGTITTIGYGNI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LALLALVILVIVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIKLLV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 ILLLIFYISYLMFGAAIYYHIE-------HGEEKISRAEQRKAQIAINEY---LL 51
                                                                                     110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EELGDKNTTTQDEILQRISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNI 111
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                                                                                   Conservative
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                                                                                                15.6%; Score 323.5; DB 2; 28.7%; Pred. No. 8.5e-14;
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29.1%;
                                                                           48; Mismatches
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                                                                              150;
                                                                           Indels
                                                                                                                         Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable potassium channel chain n2P38 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AF083652; PIDN:AAC32863.1
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A; Residues: 1-329 <WAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: Potassium channels
A; Reference number: Z22450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
223 SLVFILFGLTVISAAMNLL--VLRFLTMNTEDERRDEQEAILAAQGLVRVGDPTA 275
                                                 236 VWFWILFGLAYFASVLTTIGNWLRAVSRRTRAEMGG-----LTAQAASWTGTVTA 285
                                                                                             163 TGWGGLLIFGGAFMFSSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQTQPEYVFF 222
                                                                                                                                               178 LIGCLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV--PGDGTGQNSPAYQPL 235
                                                                                                                                                                                              114 ALAGIPLGLIMFQSIGERMNTFAAKLLRFIRRAAG------KQPIVTSSDLIIFC 162
                                                                                                                                                                                                                                               125 ALVGIPLFGMLLAGVGDRLGS-----SLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFL 177
                                                                                                                                                                                                                                                                                              60 EIL-----EATIVKSVPHKAGYQWKFSGAFYFATTVITTIGYGHSTPMTDAGKVFCMLY 113
                                                                                                                                                                                                                                                                                                                                           67 EALGGGANPETSWTNSSNHSSA--WNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 PSS------PGVVRGGQAP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 ESSDTQSERGCALPRAPRGRRRP 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 APESRGLWLPR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 WILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTARVTQRTGPSAPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 LLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV----PGDGTGQNSPAYQPLVWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 FYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIE-AIFLKWHVPPGLVRSLSAVLFLLIGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                               9 LSLIVCTLTYLLVGAAVFDALETENEILQRKLVQRVREKLKTKY----NMSNADY----- 59
                                                                                                                                                                                                                                                                                                                                                                                                                           7 LALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIKLLV 66 | 1:1: | 1: | 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z.W.; Salkoff, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVAFSFLYILLGLTVIGAFLNLVVLR-----FLVASADWPERAA-----RTPSPRPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATLALGAVAFSHFEGWTFFHAYYYCFITLTTIGFGDFVALQSGEALQRKLP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FYALLGIPLTLYTFQSLGERLNAVVRRLLLAAKCCLGLRW----TCVSTENLVVAGLLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EL--ERLALQAEPHRA-----GRQWKFPGSFYFAITVITTIGYGHAAPGTDSGKVFCM 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVRAAGLVLCTLCYLLVGAAVFDALESEAESGRQRLLVQKRGALRRKFGF----SAEDYR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PEKEQPLLPSSLPAPPAVVEPAGRPGSPA---PAEKVETPSPPTASALDYPSENLAFID 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.5%; Score 322; DB 2; 31.5%; Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --RPARSVGSASVFCHVHKLERCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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9;

outward rectifier potassium channel homolog $\mathsf{twk}\text{-}23$ - Caenorhabditis elegans C;Species: Caenorhabditis elegans

T32347

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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32347
R;Murray, J; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F34D6.
A;Reference number: Z21153
A;Accession: T32347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL;AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.3
A;Experimental source: strain Bristol N2; clone F34D6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
T43361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: twk-23; CESP:F34D6.3
A;Map position: 2
A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3
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                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-364 <WAN>
A;Cross-references: EMBL:AF083646; PIDN:AAC32857.1
                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Description: Potassium channels in C. elegans.
A;Reference number: 22450
A;Accession: T43361
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable potassium channel chain n2P20 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan 2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
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A; Residues: 1-336 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T43361
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local :
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  122 IFYALVGIPLFGMLLAGVGDRLGSSLR-----RGIGHIEAIFLKWHVPPGLVRSLSAVL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LLVEALGGGANPETSWTNSSNHSSA--WNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFC 121
                                                   66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 ---EIL-----EATIVKSVPHKAGYQWKFSGAFYFATTVITTIGYGHSTPMTDAGKVFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                               2 RSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFFSLVFILFGLTVISAAMNLL--VLRFLTMNTEDERRDEQEAILAAQGLVRVGDPTA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPLVWFWILFGLAYFASVLTTIGNWLRAVSRRTRAEMGG-----LTAQAASWTGTVTA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFCTGWGGLLIFGGAFWESSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQTQPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFLLIGCLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV--PGDGTGQNSPAY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLYALAGIPLGLIMFQSIGERMNTFAAKLLRFIRRAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFYALVGIPLFGMLLAGVGDRLGS-----SLRRGIGHIEAIFLKWHVPPGLVRSLSAV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSLIVCTLTYLLVGAAVFDALETENEILQVRGLGEPRKLVQRVREKLKTKYNMSNADY--
                                                   EAIAIKSIPQQAGYQ------WQFAGAFYFATVVITTVGYGHSAPSTNAGKLFC
                                                                                               IKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFC 121
                                                                                                                                                   KSARALLLILSTFTYLLFGAMVFDKLESEKDTWVRDEIERITDR-LKHKYNFSERDLHLF 65
                                                                                                                                                                                                                                                      103;
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                      66;
                                                                                                                                                                                                                                                                           Score 298.5; DB 2; Pred. No. 3.8e-12;
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                      154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 336;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                  Length 364;
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RESULT T21834

hypothetical protein F36A2.4 - Caenorhabditis elegans

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RESULT
T19860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C40C9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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A; Gene: CESP: C40C9.1
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A; Residues: 1-334 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z19188
A; Accession: T19860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T19860 R; Hembry, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone C40C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:270266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 MIFALFGVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVS----
                                                                                                                                                                          171
                                                                                                                                                                                                                                                               114 MIFALFGVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVS--- 170
                                                                                                                                                                                                                                                                                                           122 IFYALVGIPLFGMLLAGVGDRLGSSLR-----RGIGHIEAIFLKWHVPPGLVRSLSAVL 175
270 SA
                                                                                                                                 234
                                           294 SA 295
                                                                                       229 FATIMFILIGLAVFSACVNLL---
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nes 82; Conserv
                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                          KSARALLLILSTETYLLFGAMVFDKLESEKDTWVRDEIERITDR-LKHKYNFSERDLHLF 65
                                                                                                                              PLVWFWILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTARVTQRTGP 293
                                                                                                                                                                                                                    FLLIGCLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTG--QNSPAYQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DVHLRRRSTRRSIQDTVCCGCFKPRPPRHRFSLTRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAIVLERFTRNSLVDSQIFNIQKHSTVGVLPGRPRRMYSI----VPNSTA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FATIMFILIGLAVFSACVNLL--------VLGFMASNADEVTA--AQREPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLVWFWILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTARVTQRTGP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LTIG-EMVIVSGTYMFHTIEKWSIFDAYYFCMITESTIGFGDLVPLQQVNALQDQPLYV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILIGCLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTG--QNSPAYQ 233
                                                                                                                                                                          -LTIG-FMVIVSGTYMFHTIEKWSIFDAYYFCMITFSTIGFGDLVPLQQVNALQDQPLYV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDESSDTQSER-----GCALPRAPRGR----RRP 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPPPEK -- EQPLLPSSLPAPPAVVEPAGRPGSPAPAEKVETPSPPTASALDYPSENLAF 351
  271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%; Score 291.5; DB 2; Length 334; 27.2%; Pred. No. 9.8e-12; ative 59; Mismatches 116; Indels 45
                                                                                       -VLGFMASNADEVTA - - AQREPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352
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Nature 368, 32-38, 1994
A:Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E tock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A:Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. A; Reference number: $43531; MUID:94150718
                                                                                                                                                                                                                                                                  hypothetical protein r39B6B.f [imported] - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                   raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, Nature 368, 32-38, 1994
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A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-392 <WIL>
                                                                                                                                                                                                      R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier,
                                                                                                                                                                                                                                                         C; Accession: T45032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
c;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21834
R;Lennard, N.
submitted to the EMBI Data Library, October 1996
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A;Map position: 1
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A; Residues: 1-528 <WIL>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z19476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LLALVLLYLVSGALVFQALEQPH------
                                                                                                                                                                                                                                                                                                                                                                                                                          RGSHVLPNEKFMFARLPPDPPSDCQVVSTSAYSVRLAWAPPFSPDP 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRKLKSSNPFYLLREAKARRRRAAMASLLAQLAK--GMIFAHKDYNELARKKSKRKKEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLIGIPLTLYTVANVAKELSETIFFLHYELWNKCLEWKRKRKGEVEADPLQPMFGDDENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALVGIPLFGMLLAGVGDRLGSSL-------RRGIGHIEAIFLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDYVDTVFYAHRAVRHGYDEDSPTWDFANSVFFTTTMLTSIGYGYVAPSTFGGRLFGVIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SALKKDHMAKIEQNAKDYVDKLWSVAKRDRDKY-----KNVEDLIKSVKEDTVDDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EQQAQKKMD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGSVVLYIILGAIVFQMLEGEHLDNFSDFNPKKHFGPKMVDKFFETIFRRWSKGANFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGPSAPPPEKEQ-PLLPSSLPAPPAVVEPA-----GRPGSPAP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNWLR-----AVSRRTRAEMGGLTAQAASWTGTVTA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILTVGFGDIRPSPGN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------WHVPPGLVRSLSAVLELLI-GCLLEVLTPTFVFSYMESWSKLEAIYFVIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPETSWT-----NSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEILDRVRLVRFPP-----LTVFFFVFVYGCI-----AAWVVRYWETWTYVESLYFIFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
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23.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---HGRDQFLRDHPCVSQKSLEDFIKLLVEALGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --IWVTLAFVVVGVILTTMCMDVVGRMYLKEIHYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413/1; 464/2;
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hypothetical protein R04F11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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T23907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 5
A; Introns: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1; 489/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-524 <WIL>
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Best Local Similarity
Thehes 75; Conserv:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP:R04F11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone R04F11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
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Best Local
    164
                                            139 VGDRLGS---SLRRGIGHIEAIF----
                                                                                       104 DVIYGDGPIKWSFMSSIFFSWTAITTIGYGHIVPRTDEGRVAIIFYALLGIPLILVTIAD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 FLATL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 VLTTI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 FSSIETDWSYLDAFYYCFVSLTTIGLGDFEPGDDPNQSFRGLYKIGATVYLMGGLCCMML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 FSYMES-WSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPAYQPLVWFWILFGLAYFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 VARMREPSHKLRGLLNQRLGH----LFTVNHI------QLIHVGVVFASLLLFVFAIPAWV
                                                                                                                                      88
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                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 FQALEQPHEQ-QAQKKMDH----GRDQFLRDHPCVSQKSLEDFIKLLVEALGGGANPETSW
                                                                                                                                                                                                                                                                                                                   7 LAL--LALVLL---YLVSGALVFQALEQPHEQQAQKK-----
                                                                                                                                                                               TAYSTWRQTANDGMDELIRD---------VFWDYTRNYMTPD 103
                                                                                                                                                                                                                                                                        LALPHFGLVLLSIGYTLIGALCFHHYEKPYEQQLRNETSRRIGELKNRVMDQLWRMSNNG 70
IGRFLATYIIKLHHGYMAVMSFVTNSCLKCIKWACCWIRLPRRHIPMPTLELLQRTQKLY 223
                                                                                                                                                                                                                         -----GRDQFLRDHPCVSQKSLEDFIKLLVEALGGGANPETSWTNSSNHSS-- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGCLLFVLT-PTFV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSDPN----WTFGQAFFFAGTLISTVGYGRVSPRTEYGKLFTILYCVIGIPLTLALLSAI 231
                                                                                                                                  ----AWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFYALVGIPLFGMLLAG 138
                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     12.9%;
23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.0%;
                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                   Score 269; DB 2;
Pred. No. 4.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 269.5; DB Pred. No. 3e-10;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                               ---LKW------HVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 524;
                                                                                                                                                                                                                                                                                                                     -----MDH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                              Indels 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                            164
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                                                                                                                                                                                                                                                                                                                                                              21;
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A;Reference number: 220027
A;Accession: T25392
A;StatUs: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T28A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25392
R:Lloyd, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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A; Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T28A8.1
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Residues: 1-393 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 PNNNNPTVAATAASAGGGTGRRKKQQRDNVSDAGTFDNISEINDGSEGGENENEGEEEEEQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 YVPPDIYYFKWIEHP-----RTLSFASDRVLQSMESLDLNTSR-CSTARTLTPR 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 GSPAPA---EKVETPSPPTASALDYPSENLAFIDESSDTQSERGCALPR--APR 371
                                                                                                                         187 T-PTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWILFGLA 245
                                                                                                                                                                                                                                                            125 TTLLTTIGYGNLTPVTGRGKLLCILYALFGVPLILITVADIGKFLSENIVQLYTWYRKLR 184
                                                                                                                                                                                                                                                                                                                                                                                               52 C--VSQKSLEDFIKLLVEALG-------GGANPETSWTNSSNHSSAWNLGSAFFFFS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                         15 VSLIVLSVVYVGFGAFLFYQLEQPNEVEVRARNIERFNIHKRQMIEHLWEMRESGIGQHV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
286 ITTMCIDLVG 295
                                                                                                                                                                                                                                                                                                                                                  75 VEDLAVKYVDNVTRILFEAFDTHCIGAKHLRPGGEDEDYNWTYM------TALFFT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LALLALVLLYLVSGALVFQALEQP-------HEQQAQKKMDHGRDQFLRDHP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQFDPSNHEKRVSVLFILLIMLGYVAGGAYIVRWWEEWTFFEAFYFCFVTVTTIGFGDIV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHLGEVFGYV-AFLQKNYGLTA-----EQLTKLSQLPEEYLLDCLINGRQPDLNWIGGRP 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQAASWTGTVTARVTQRTGPSAPPPEKEQPLLPSSLP-----APPAVVEPAGRP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA----NVDWLPATLAYIVFGLIITTMCIDLVGSEYIRDIHFYGRSLGRQFMTIGGKV 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGDGTGQNSPAYQPLVWFWILFGLAYFASVLTTIGN-WLRAVSRRTRA-----EMGGLT 273
                                            YFASVLTTIG 255
                                                                                      TFGAVVLSMWEGWDFFSGFYFSFITMTTVGFGDIVP-----LKREYYILDLCYIIIGLS
                                                                                                                                                                        EKCSKQKYSVISSKDDKNKEGDLNLDHLE------NYISIPIFLIVAILLSYI 231
                                                                                                                                                                                                                                                                                                        GTIITTIGYGNIVLHTDAGRLFCIFYALVGIPLFGMLLAGVGDRLGSSLRR------ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AVLFLLIGCLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.7%; Score 265; DB 2; Length 393; 24.8%; Pred. No. 5.8e-10;
                                                                                                                                                                                                                       ------GIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGCLLFVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
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hypothetical protein F31D4.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Mortimore, B. submitted to the EMBL Data Library, March 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z92832; PIDN:CAB07375.1; GSPDB:GN00023; CESP:F31D4.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-443 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone F31D4
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                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T24265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T01B4.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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                                                                                                                    A; Map position: X
A; Introns: 95/3; 142/1; 224/3; 290/1; 458/1
                                                                                                                                                                                                            A;Cross-references: EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4.1
A;Experimental source: clone T01B4
                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-522 <WIL>
                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                  A; Gene: CESP: T01B4.1
                                                                                                                                                                                            C; Genetics
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                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 HIYPMTDAGRMLTMIFALFGIPLMLLVLQDFGKLLTITMK------FPWFQTKRLM 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 NIVLHTDAGRLFCIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 LLESFYFFFTSLSTVGLGDLVP-----SSPRLLTMFGFILVGL----SLVSMVINLLQ 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 KLEAIYEVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWILFGLAYFASVLTTIGNWLR 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 AVSRRT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 LIIVELIYCISGGLVFWLIEEPYQSELRDAWQHKIENNRTARVDAMMKKIFNNSDYLIYI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 AKMKST 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 KGNTSQRLTTFFI----EELGSYENQLGVKW----SQQKMDWDFWNAVLFAGTICTTIGYG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 HPCVSQKSLEDFIKLLVEALGGGANP-ETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 12.6%; Score 261.5; DB 2; Local Similarity 27.5%; Pred. No. 1.1e-09; es 84; Conservative 49; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LLALVLLYLVSGALVFQALEOPHEQQAQ------KKMDHGRDQFLRD 49
                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRIMRCCTKQPIEEMKEIERQERHDLDIFDLPLPVGIAL-IVTWIFICSFVLSVWDHNWT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSLSAV-----
12.4%; Score 257.5; DB 2; 26.1%; Pred. No. 2.4e-09; ative 42; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------ESWS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                      Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
               10;
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Matches

79;

Conservative

Indels

95;

Gaps

	/ LALLALVLLTLYSGALVFQALEQPHEQQAQKKMDHGRDQFL47
0 5	39 IMLILILLGYACLGGYMFQALEYDQQQLELEAEKRVRLSESSLLAVNLLEHLKQMNCGQS 98
	99 NEKRCL-ELITKTFIQRSDEERGEGWRWDFWNSVFFSATIFTTIGY 143
Qy 1 Db 1	
Qу 1 Db 2	154IEAIFLKWHVPPGLVRSLSAVLFLLIGCLLFVLT 187
Qy 1:	ων
Qy 2,	ASV 250
Db 303 AM RESULT 14 T28933 hypothetical C;Species: Cc C;Date: 29-Oc C;Accession: C;Nelson, J.	03 AMV 305 14 14 tical protein C52B9.6 - Caenorhabditis elegans es: Caenorhabditis elegans 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000 sion: T28933
submitted to A;Description A;Reference A;Accession:	submitted to the EMBL Data Library, July 1996 A;Description: The sequence of C. elegans cosmid C52B9. A;Reference number: Z20545 A;Accession: T28933 A;Accession: T28933
A; Residues: 1- A; Cross-refere A; Experimental C; Genetics:	A;Residues: 1-513 - NEL> A;Residues: 1-513 - NEL> A;Cross references: EMBL:U64598; PIDN:AAC47976.1; GSPDB:GN00028; CESP:C52B9.6 A;Experimental source: strain Bristol N2; clone C52B9 2;Genetics:
A;Gene: CES A;Map posit A;Introns:	CESP:C5289.6 sition: X s: 12/3; 54/3; 90/3; 158/1; 173/1; 227/3; 299/3; 346/2; 378/2; 405/1; 452/3
Query Ma Best Loc Matches	Watch 12.0%; Score 248.5; DB 2; Length 513; Local Similarity 24.6%; Pred. No. 8.8e-09; res 79; Conservative 48; Mismatches 107; Indels 87; Gaps 10;
טט פ	7 LALLALVILYIVSGALVFQALEQPHEQQAQKKMDHGRDQFLRD-HPCVSQKSLEDFIKIL 65 : : : : : : : : : : : : :
)y 66 b 117	VEALGGGANPETSWTNSSNHSSA-WNLGSA : : FQAYRNQFITAKHLLNKTREDEVLWTFPNS
y 110 b 177	
y 151 b 237	1IGHIEAIFLKWHVPPGLVRSLSAVLFLLIGC 181 : : : : : : : : : : : : : :
у 182	LLEVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWIL
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A;Molecule type: DNA
A;Residues: 1-1910 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A; Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A; Reference number: A75000; MUID:99069613; PMID:9851916

A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A; Accession: H88124
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A; Gene: T12C9.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:chr_II; PIDN:AC71141.1; PID:g1086770; GSPDB:GN00020; CESP:T12C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein T12C9.3 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: H88124
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439 KSEVPVLMVFTIILLYIAFGGILFSILEDWSYMDAFYYSFISLTTIGFGDIVP 491
                            173 ----AVLELLIGCLLEVLTPTEVESYMESWSKLEAIYEVIVTLTTVGEGDYVP 221
                                                                                                                                                         143 LG-----SSLRRGIGHIEAIFLKWHVPPGLVRSLS-------
                                                                                                   382 LSECTIWLYKHMRKGSARLDSAWKRFR---GLEDSISDDLESASKNQDSSILDMDMDEID 438
                                                                                                                                                                                                               322 RGSEKMWTTSSALFFAATTMATIGYGNIVPVTPLGRLACVLFALFGAPIAIITIGDLGKF 381
                                                                                                                                                                                                                                                                                                                                                                                                                                  202 IVLVVCVCTYATIGAWIFYTLESPNEDRLKETGRKTIAEMRSNLIYKINNNEKEVWKEDI 261
                                                                                                                                                                                                                                                                                                                         262 EKELMLYSEKLYKAFKEQYVRYSDVRTIGFEGRSSYEEADETGGDSERKRRHRHGNKRGD 321
                                                                                                                                                                                                                                            86 ----SSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFYALVGIPLFGMLLAGVGDR 142
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342 FGLSLATMCIDLAGTEYIRKI 362
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Search completed: June 4, 2002, 11:01:02 Job time: 137 sec

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Perfect score:
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Maximum Match 100%
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1: sp_archea:*
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6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	14	-				9	89	7	60	Si	4	ω ~	2	1 16	Result No. S
370.5 365	376.5	376.5	390	415.5	421	128.5	133.5	490	195.5	768.5	768.5	76.5	969	1692.5	Score
17.8	18.1	18.1	18.8	20.0	20.3	20.6	20.9	23.6	23.8	37.0	37.0	37.3	46.6	81.4	Query Match
259	336	336	313	241	502	332	343	294	309	426	370	411	186	419	Query Match Length DB
40	. 11	11	11	11	11	4	4	4	4	11	11	4	11	4	DB.
Q9H59Z 002821	Q99L99	Q9Z2T2	Q9ERU5	Q9CX88	Q9JK62	Q96T54	Q9BXD1	Q9H591	Q96T55	Q920B6	Q924T4	Q9NRT2	Q925Q7	Q96T94	ID
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ALIGNMENTS

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O9NRT2:

01-OCT-2000 (TrEMBLrel. 15, Created)

01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.
                                                                       Q9NRT2
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ozalia A., Vega-Saenz de Miera E.C.;
"Cloning of Two transcripts of the Human 2-Pore K+ channel KT4.1 Gene. Chromosomal Localization, Tissue Distribution and Functional Expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last seque 01-DEC-2001 (TrEMBLrel. 19, Last annot TWO PORE K+ CHANNEL KT4.1 (FRAGMENT).
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01-DEC-2001 (TrEMBLrel.
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STRAIN-SPRAGUE-DAWLEY;
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                                                                                                                                                           394 KAVPV 398
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                                                                                                                                                                                                                                   AQAASWTGTVTARVTQRTGPSAPPPEKEQPLLPSSLPAPPAVAEPAHRPGSPAPAEKVET
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19, Last sequence update)
19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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Pred. No. 2.1e-64;
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         STRAIN-SPRAGUE-DAWLEY;
MEDLINE=21268449; PubMed=11374070;
MEDLINE=21268449; PubMed=11374070;
Kim Y., Bang H., Gnatenco C., Kim D.;
"Synergistic interaction and the role of C-terminus in the activation of TRAKK K+ channels by pressure, free fatty acids and alkali.";
Pflugers Arch. 442:64-72(2001).
EMBL; AF302842; AAK60504.1; -.
                                                                                                                                                                                                                                                   Q92414;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                             MECHANOSENSITIVE TANDEM PORE POTASSIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                       Q924I4
                                                                                                                                                                            NCBI_TaxID=10116;
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Pflugers Arch. 439:714-722(2000).
EMBL; AF171068; AAF89743.1;
InterPro; IPR003280; 2poreK_channel.
InterPro; IPR000358; Cation_chan_non_lig.
InterPro; IPR000658; Cation_chan_non_lig.
InterPro; IPR001622; Channel_pore_K.
InterPro; IPR003976; Trek_channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20244931; PubMed=10784345;
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   channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chapman C.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 776.5; DB 4
Pred. No. 9.5e-50;
                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                   370 AA
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                                                                                                                                                                                                                                                            update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 411;
                                                                                                                                                                                      Murinae; Rattus
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SEQUENCE

370 AA;

40874 MW;

54677E351CE64234 CRC64;

Local Similarity

37.0%; Score 768.5; DB 1 49.5%; Pred. No. 3.3e-49;

DB 11; Length 370; 84; Indels

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57; Mismatches

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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat)
2D DOMAIN POTASSIUM CHANNEL KCNK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bockenhauer D., Zilberberg N., Goldstein S.A.;
"KCNKZ: reversible conversion of a hippocampal potassium leak into voltage-dependent channel.";
vat. Neurosci. 4:486-491(2001).
EMBL; AF325671; AALO1159.1;
Ionic channel.
Ionic channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CLLFYLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21219399; PubMed=11319556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 LVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FIKLLVEALGGGANPETSWINSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHIDAGRLF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 MKWKTVSTIFLVVVLYLIIGATVFKALEQPQEISQRTTIVIQKQNFIAQHACVNSTELDE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                               117 LIQQIVTAINAGIIP---LGNNSNQVSHWDLGSSFFFAGTVITTIGFCNISPRTEGGKIF 173
                                                                                                                                       121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180
181 CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI 240
                                                                                                                                                                                                                                  61 FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141; Conservative
                                                                                                                                                                                                                                                                                 MKWKTVSTIFLVVVLYLIIGATVFKALEQPQEISQRTTIVIQKQNFIAQHACVNSTELDE 116
                                                                                          CITYALLGIPLFGFLLAGVGDQLGTIFGKGTAKVEDTFIKWNVSQTKIRIISTIIFILFG 233
                                                                                                                                                                                                                                                                                                                                                                                 141;
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 AA; 46912 MW; CACDA05BBE95FDBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     37.0%; Score 768.5; DB 11; Length 426; 49.5%; Pred. No. 3.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                      57; Mismatches
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01-DEC-2001
01-DEC-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2P DOMAIN POTASSIUM CHANNEL TALK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Girard C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain K+ channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lazdunski M., Lesage F.;
"Genomic and functional characteristics of novel human pancreatic 2P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                09H591;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DJ137F1.2 (NOVEL MEMBER OF THE POTASSIUM CHANNEL SUBFAMILY K).
DJ137F1.2.
                                                                                                                                                   Q9H591
                         Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                    130 LLGIPLNVIFL----NHLGTGLRAHLAAIE----RWEDRPRRSQVLQVLGLALFLTLGTL 181
                                                                                                                                                                                                                                                                                                                                                                                                              126 LVGIPLEGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPP---GLVRSLSAVLFLLIGCL 182
                                                                                                                                                                                                                                                                          242 IGLAWLALIL-PIGPLLIHRCCQLWLLSLRQ------GCGAKAAPGRRPRRGSTAARGV 293
                                                                                                                                                                                                                                                                                                   242 FGLAYFASVLTTIGN------WLRAVSRRTRAEMGGLTAQAASW----TGTVTARVT 288
                                                                                                                                                                                                                                                                                                                               182 VILIEPPMVESHVEGWSESEGEYFAFITLSTIGFGDYVVGTDPSKHYISVYRSLAAIWIL 241
                                                                                                                                                                                                                                                                                                                                                         183 LFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPG-DGTGQNSPAYQPLVWFWIL 241
             NCBI_TaxID=9606;
                                                    Homo sapiens (Human)
                                                                                                                                                                                                                        294
                                                                                                                                                                                                                                                                                                                                                                                                                                          66 VEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTITTTIGYGNIVLHTDAGRLECIFYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 VLPLLLAYVCYLLLGATIFQLLEROAEAQSRDQFQLEKLRFLENYTCLDQWAMEQFVQVI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                      QVTPQDFPISKK 305
                                                                                                                                                                                                                                                 QRTGPSAPPPEK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 AA; 34153 MW; 99C4B11EB26B0764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Res. Commun. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.8%; Score 495.5; DB 4; Length 309; 37.2%; Pred. No. 4.4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terrenoire C., Tinel N., Fosset M., Romey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                 Hominidae;
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                                                                                          Matches 111;
                                                                                                                                                  Query Match
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                                                                                                                                                                                                 EMBL; AF339912; AAK28551;;
InterPro; IPR003280; 2poreK_channel.
InterPro; IPR000636; Cattion_chan_non_lig.
InterPro; IPR001622; Channel_pore_K.
Pfam; PF00520; ion_trans; 1.
PRINTS; PR01333; 2POREKCHANEL.
SEQUENCE 343 AA; 38172 MW; 29B1F354CE22E3BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9EXD1;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POTASSIUM CHANNEL TASK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-ADRENAL GLAND;
MEDLLINE-21145510; PubMed=11248242;
Decher N., Maier M., Dittrich W., Gassenhuber J., Bruggemann A.,
                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of TASK-4, a novel member of the pH-sensitive, pore domain potassium channel family."; FEBS Lett. 492:84-89(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Busch A.E., Steinmeyer K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BXD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                      Local Similarity
5 TLLALLALVILYIVSGALVFQALEQPHEQQAQKKMDHGRDQFIRDHPCVSQKSLEDFIKL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL136087; CACO7336.1; ...
InterPro; IPR003280; 2poreK_channel.
InterPro; IPR003636; Catchon_chan_non_lig.
InterPro; IPR001622; Channel_pore_K.
Pfam; PF00520; ion_trans; 1.
PRINTS; PR01333; 2POREKCHANEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 FGLAYFASVL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 VILIFPPMVFSHVEGWSFSEGFYFAFITLSTIGFGDYVVGTDPSKHYISVYRSLAAIWIL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 LFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPG-DGTGQNSPAYQPLVWFWIL 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Williams S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 MEAWVKGVNPKGNSTNPSN----WDFGSSFFFAGTVVTTIGYGNLAPSTEAGOVFCVFYA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 VEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 VLPLLLAYVCYLLIGATIFQLLERQAEAQSRDQFQLEKLRFLENYTCLDQWAMEQFVQVI 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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NCE 294 AA; 32507 MW; FCBA3B352F1F0952 CRC64;
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                 20.9%; Score 433.5; DB 4
36.2%; Pred. No. 1.9e-24;
ative 49; Mismatches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.6%; Score 490; DB 4; Length 294; 40.8%; Pred. No. 1.1e-28; ative 54; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 AA
                                                                                                                            DB 4;
                                                                    Indels
                                                                                                                               Length
                                                                    27;
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                                                              Gaps
                                                           7;
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                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
252 GMAWLALIIKLILSQLETPGRVCSCCHHSSKEDF----KSQSW-----RQGPDR 296
                                243 GLAYFASVLTTIGNWLRAVSR------RTRAEMGGLTAQAASWTGTVTARVTQRTGPSA 295
                                                                  192 FLLLPPLLFSHMEGWSYTEGFYFAFTTLSTVGFGDYVIGMNPSQRYPLWYKNNVSLWILF
                                                                                                184 FVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPA-YQPLVWFWILF 242
                                                                                                                                  136 FALVGIPLNLVVL----NRLGHLMQQGVNHWASRLGGTWQDPDKARWLAGSGALLSGLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. EMBL; AF358910; AAK49533.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                  124 YALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGCLL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain K+ channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tazdunski M., Lesage F.;
"Genomic and functional characteristics of novel human pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Girard C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q96T54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q96T54
                                                                                                                                                                                                    80 DVVQAYKNGA----SLLSNTTSMGRWELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIF 135
                                                                                                                                                                                                                                    64 LLYEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIF 123
                                                                                                                                                                                                                                                                    21 STVLLLLA-YLAYLALGTGVFWTLEGRAAQDSSRSFQRDKWELLQNFTCLDRPALDSLIR 79
                                                                                                                                                                                                                                                                                                     4 TTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 PHSKDAI 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 MA-----WLALISNSSSPSWRRQGGYVPAATTALRKTSSPKAGDRDLTGSQSPT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 LAYFASVLTTIGNWLRAVSRRT----RAEMGGLTAQAASWTGTVTARVTQR--TGPSAPP 297
                                                                                                                                                                                                                                                                                                                                                                          rocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 LLLPPLLFSHMEGWSYTEGFYFAFITLSTVGFGDYVIGMNPSQRYPLWYKNMVSLWILFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 VLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPA-YQPLVWFWILFG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 ALVGIPLFGMILAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGCILF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 VVQAYKNGA----SLLSNTTSMGRWELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIFF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 LVEALGGGANPETSWINSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 TVLLLLA-YLAYLALGTGVFWTLEGRAAQDSSRSFQRDKWELLQNFTCLDRPALDSLIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                       111;
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                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            332 AA; 36894 MW; 1848DBC06E078158 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,
                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                            20.6%; Score 428.5; DB 4; Length 332; 36.0%; Pred. No. 4.4e-24;
                                                                                                                                                                                                                                                                                                                                                   49;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Best Local :
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cid L.P., Niemeyer M.I., Sepulveda F.V.;
"Functional properties of mouse TASK-2 potassium channel.";
submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF259395; AAF68668.L; -.
EMBL; AF319542; AAG35065.l; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9JK62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roux J., Barhanin J.;
"Mouse two P domain potassium channel TASK2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-129/SVJ; TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003280; 2poreK_channel.
InterPro; IPR003636; Cation_chan_non_lig.
InterPro; IPR001623; Channel_pore_K.
InterPro; IPR001623; Channel_pore_K.
P£am; PF00520; 1on_trans; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                               123 VPLCLTWISALGKFFGGRAKRLGQFLTRRGVSLRKAQITCTAIFIVW------ 169
                                                                                                                                                                        234 PLVWFWILFGLAYFASVLTTIGNWL-----RAVSRRTR------AEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
341 ASL-APLVVYSKNRVPSLEEVSQTLKNKGHVSRPLGEEAGAQAPKDSYQTSEVFINQLDR 399
                                   307
                                                                    281 GSTASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGERVPGPGHGLGPQGDRLPTIP
                                                                                                                                                                                                                                                                                                                                                                                        69
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                                                                                                                                       YFVELWIYLGLAW----LSLFVNWKVSMFVEVHKAIKKRRRRKESFESSPHSRKALQMA 280
                                                                                                                                                                                                                                               LFLLIGCLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPA-YQ 233
                                                                                                                                                                                                                                                                                                                  IPL-----FGMLLAGVGDRLGSSL-RRGIG-----HIEAIFLKWHVPPGLVRSLSAV 174
                                                                                                                                                                                                                                                                                                                                                                                        LGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFYALVG 128
                                                                                                                                                                                                                                                                                                                                                                                                                          LTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLSQEGLDKILQVVSDA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIKLLVEA 68
                                                                                                                                                                                                                                                                                                                                                   ----ADQGVAITGNQTENN-WNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFG 122
                                                                                                                                                                                                              ----GVLVHLVIPPFVFMVTEEWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYR
                                   SSLPAP-----PAVVE-----PAG-RPGSPAPAEKVET-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      502 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.3%; Score 421; DB 11; 26.8%; Pred. No. 2.6e-23;
                                                                                                       -QAASWTGTV----TARVTQRTGPSAP-----PPEKEQPLLP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E4C7E7CC71B44D95 CRC64;
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RESULT 11
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RP STRAIN-C578L/6J; FISSUE-EMBRYONIC HEAD;

RX MEDIINE-21085660; PubMed=11217851;

RX MEDIINE-21085660; PubMed=11217851;

RX MEDIINE-21085660; PubMed=11217851;

RX MARANA T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Rodota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Rohirah P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl R., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Asaski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Havashiraki Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9CX88;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3010005K24RIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
EMBL; AK019376; BAB31686.1; -.
MGD; MGI:1924704; 3010005K24Rik.
Interpro; IPR001622; Channel_pore_K.
SEQUENCE 241 AA; 25799 MW; B4C39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 GP 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 ISEEGEPWEALDYHPLIFQNANITFENE-----ETGLSDEETSKSSVEDNLTSKEQPEQ 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 --PSPPTASALDY-----PSENLAFIDESSDTQSERGCALPRAPRGRRRPNPSKKPSRPR 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.
                                                                                                                                                                               127 LIQHALDADNAGVSPV---GNSSNSSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 183
    226
                                                                                            184
                                              181 CLLFVLTPTFV 191
                                                                                                                                                                                                                             61 FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120
                                                                                                                                                                                                                                                                            67 MKWKTVVAIFVVVVYLVTGGLVFKALEQPFESSQKNTIALEKAEFLRDHICVSPQELET 126
                                                                                                                                                                                                                                                                                                                       1 MRSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GP
    C--FVCTHIFV 234
                                                                                                                                   CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180
                                                                                            CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVF-RAH---
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                20.0%; Score 415.5; DB 1 46.1%; Pred. No. 2.8e-23;
                                                                                                                                                                                                                                                                                                                                                                             32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B4C39F77CD0A39DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 241;
                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 13
Q9Z2T2
ID Q9Z2T2
AC Q9Z2T2
DT 01-MAY
DT 01-OCT
DE PUTATT
OS RATTUS
OC EUKARY
OC MAMMAL
OX NCBL_T;
RN [1]
RP SEQUENC
RA Gan L.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                       09ZZTZ;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE POTASSIUM CHANNEL TWIK.
                  SEQUENCE FROM N.A.
                                                   Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                             Q9Z2T2
                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "TWIK-2, an inactivating 2P domain K+ channel.";
J. Biol. Chem. 275:28722-28730(2000).

EMBL; AF281304; AAG10508.1;
InterPro; IPR003280; 2poreK_channel.
InterPro; IPR00056; Cation_chan_non_lig.
InterPro; IPR001622; Channel_pore_K.
InterPro; IPR001779; TWIK1_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01333; 2POREKCHANEL. PRINTS; PR01096; TWIK1CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SPRAGUE-DAWLEY;
MEDLINE=20435832; PubMed=10887187;
                                                                                                                                                                                                                                                                          237
                                                                                                                                                                                                                                                                                               235 LVWFWILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00520; ion_trans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patel A.J., Maingret F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CT-2001 (TrEMBLrel. 18, Last annotation update)
2P DOMAIN K+ CHANNEL TWIK-2.
                                                                                                                                                                                                                                                                                                                                                                                     119 GKAFSIVFALLGVPITMLLLTASAQRL--SLLLTHAPLSWLSLRWGWHPQRAARWHLVAL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ionic channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Honore E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ERU5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ERU5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 ALLALVIL----YLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 RVLAAGRLGRAVLANASGP----ANASD--PAWDFASALFFASTLVTTMGYGYTTPLTDA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 LLVEA------LGGGANPETSWINSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ഗ
                                                                                                                                                                                                                                                                                                                           LMVIVAIFFLIPAAVFAYLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRSLYKV
                                                                                                                                                                                                                                                                                                                                                       LLIGCLLFVLTPTFVFSYM-ESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQ-NSPAYQP 234
                                                                                                                                                                                                                                                                                                                                                                                                                    GRLFCIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLF 176
                                                                                                                                                                                                                                                                   LVTAYLFLGLVAMVLVLQTF-----RRVSDLHGLT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLASALVAYAGYLALGALLVARLERPHEARLRAELGTLREQULRHSPCVAAHALDAFVE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
   Joiner W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 AA;
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34214 MW; A93629568785CD8F CRC64;
   Quinn A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.8%; Score 390; DB 11; 35.1%; Pred. No. 2.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnone V., Fosset M., Lazdunski M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
                                                              Sciurognathi;
                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi; Muridae;
Wang L.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                         336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                            Muridae;
Hughes T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                            Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
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ACCOMENS TO THE PROPERTY OF TH
                                                                                                      A Strausberg R.;

A Strausberg R.;

L Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC003729; AAH03729.1; -.

R MGD; MGI:109322; Kcnkl.

PR InterPro; IPR003280; 2poreK_channel.

PR InterPro; IPR00636; Cation_chan_non_lig.

DR InterPro; IPR001622; Channel_pore_K.

DR InterPro; IPR001779; TWIK1_channel.

DR Pfam; PF00520; ion_trans; 1.

DR PF1NTS; PR01333; 2POREKCHANEL.

DR PRINTS; PR01333; 2POREKCHANNEL.

SQ SEQUENCE 336 AA; 38201 MW; 76B7FD5361A6216C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
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                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCNK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTASSIUM CHANNEL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99L99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00520; ion_trans; 1.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01096; TWIKICHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 YKIGITCYLLLGLIAMLVVLET 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 LGFVTVSCFFFI--PAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFREL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 --FLLIGCLLFVLTPTFVFSYME-SWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 GKAFCIIYSVIGIPFTLLFLTAVVQRVTVHVTRRPVLYFH---IRWGFSKQVVAIVHAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003280; 2poreK channel.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001622; Channel_pore_K.
InterPro; IPR001779; TWIK1_channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 YQPLVWFWILFGLAYFASVLTT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaczmarek L.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 FLGRVLEASNYGVSVLSNASGNWN------WDFTSALFFASTVLSTTGYGHTVPLSDG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIKLLVEALGGG----ANPETSWINSSNHSSAWNLGSAFFFSGIIITIIGYGNIVLHTDA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRLFCIFYALVGIPLFGMLLAGVGDRLGSSL-RRGIGHIEAIFLKWHVPPGLVRSLSAVL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSAWCFGFLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY
                            18.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38228 MW; 5E78031947D75DE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.1%;
Score 376.5;
Pred. No. 3.2e
53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K, MEMBER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 376.5; DB 1
Pred. No. 3.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96;
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9

Matches

Conservative

53;

. 3.2e-20;

Indels Length 336;

23;

9;

DB 11;

Best Local Similarity

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RESULT
Q9H592
ID Q9
DT Q1
DT Q
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ionic channel.
NON_TER 22
SEQUENCE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09H592 PRELIMINARY; PRT; 229 AA.
09H592;
01-MAR-2001 (TrEMBLrel 16, Created)
01-MAR-2001 (TrEMBLrel 16, Last sequence update)
01-UN-2001 (TrEMBLrel 17, Last annotation update)
01-UN-2001 (TrEMBLREL 17, Last annotation update)
DJ137F1.1 (NOVEL MEMBER OF THE POTASSIUM CHANNEL SUBFAMILY K )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hòmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003280; 2poreK_channel.
InterPro; IPR001622; Channel_pore_K.
PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Williams S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT).
DĮ137F1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2000) to the EMBL/GenBank/DDBJ EMBL; AL136087; CAC07335.1; -.
         192
                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 LGFVTVSCFFFI--PAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 YKIGITCYLLLGLIAMLVVLET 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 YOPLVWFWILFGLAYFASVLTT 253
                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                           64 LLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 40.6 nes 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                    4 TTLLALVLALVLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
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                                                                                                                                                                           YALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGCLL 183
                                                                                                               FALVGIPLNLVVL----NRLGHLMQQGVNHWASRLGGTWQDPDKARWLAGSGALLSGLLL 191
                                                                                                                                                                                                                                           DVVQAYKNGA----SLLSNTTSMGRWELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKAFCIIYSVIGIPFTLLFLTAVVQRVTVHVTRRPVLYFH---IRWGFSKQVVAIVHAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRLFCIFYALVGIPLFGMLLAGVGDRLGSSL-RRGIGHIEAIFLKWHVPPGLVRSLSAVL 175
FLLLPPLLFSHMEGWSYTEGFYFAFITLSTVGFGDYV
                                                            FVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FLLIGCLLFVLTPTFVFSYME-SWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLGRVLEASNYGVSVLSNASGNWN------WDFTSALFFASTVLSTTGYGHTVPLSDG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIKLLVEALGGG----ANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDA 116
                                                                                                                                                                                                                                                                                                                                                                 STVLLLLA-YLAYLALGTGVFWTLEGRAAQDSSRSFQRDKWELLQNFTCLDRPALDSLIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSTTLLALLAL-VLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSAWCFGFLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
25344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.8%; Score 370.5; DB 4; Length 229; 40.6%; Pred. No. 5.6e-20; tive 37; Mismatches 83; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7AB9FB847F242ECE CRC64;
   228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
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